

SEQUENCE LISTING



<110> Shimkova, Richard A.

<120> NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES

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<140> 09/991,053

<141> 2001-11-21

<150> USSN 60/123,667

<151> 1999-03-09

<150> 09/520,731

<151> 2000-03-08

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<170> PatentIn Ver. 2.1

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aaagattata taatatttaa atccacatag atctattctt aagctgaatg aacattactt 1725

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Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
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Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
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Ser Glu Pro Ile Ser Ile Ser His Gly Asn Tyr Thr Lys Gln Tyr Pro
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Val Phe Val Gly His Lys Pro Gly Arg Asn Thr Thr Gln Arg His Arg
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Leu Asp Ile Gln Met Ile Met Ile Met Asn Gly Thr Leu Tyr Ile Ala
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Ala Arg Asp His Ile Tyr Thr Val Asp Ile Asp Thr Ser His Thr Glu
75 80 85

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Glu Ile Tyr Cys Ser Lys Lys Leu Thr Trp Lys Ser Arg Gln Ala Asp
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Val Asp Thr Cys Arg Met Lys Gly Lys His Lys Asp Glu Cys His Asn
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tca gcc aca ggg act gac ttc ctt gcc att gac gca gtc att tac ccg 810

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Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ile	Ala	Val	Glu	Tyr	Asn	Thr	Met	Gly		
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Lys	Val	Val	Phe	Pro	Arg	Val	Ala	Gln	Val	Cys	Lys	Asn	Asp	Met	Gly		
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Arg	Leu	Asn	Cys	Ser	Val	Pro	Gly	Asp	Ser	His	Phe	Tyr	Phe	Asn	Ile		
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ctc	cag	gca	gtt	aca	gat	gtg	att	cgt	atc	aac	ggg	cgt	gat	gtt	gtc		1146
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Lys	Gln	Gln	Lys	Ser	Pro	Asp	Ser	Thr	Trp	Thr	Pro	Val	Pro	Asp	Gln		
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Tyr Asn Ser Glu Lys Cys Ser Tyr Asp Gly Val Glu Asp Lys Arg Ile	475	480	485
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Gln Lys Gln His
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370 375 380

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 Ala Gln His Gly Tyr His Ser Arg Gly Gly Met Leu Arg Trp Lys His
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725 730 735

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740 745 750

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755 760 765

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770 775 780

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785 790 795 800

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820 825 830

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835 840 845

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850 855 860

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 Met Arg Ser Glu Ala Leu Leu
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 Leu Tyr Phe Thr Leu Leu His Phe Ala Gly Ala Gly Phe Pro Glu Asp
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 Ser Glu Phe Ile Ser Ile Ser His Gly Asn Tyr Thr Lys Gln Tyr Pro
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Phe Ile Lys Val Leu Leu Lys Lys Asn Asp Asp Ala Leu Phe Val Cys	
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Asp Ala Lys His Ala Asn Val Ala Leu Phe Ala Asp Gly Lys Leu Tyr	
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Ser Ala Thr Val Thr Asp Phe Leu Ala Ile Asp Ala Val Ile Tyr Arg	
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Ser Leu Gly Glu Ser Pro Thr Leu Arg Thr Val Lys His Asp Ser Lys	
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Trp Leu Lys Glu Pro Tyr Phe Val Gln Ala Val Asp Tyr Gly Asp Tyr	
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Ile Tyr Phe Phe Phe Arg Gln Ile Ala Val Gln Tyr Asn Thr Met Gly	
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Lys Val Val Phe Pro Arg Val Ala Gln Val Cys Lys Asn Asp Met Gly	
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Asn Ser Gly Phe Leu Asn Asp Ser Leu Phe Leu Glu Glu Met Ser Val	
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Tyr Asn Ser Glu Lys Cys Ser Tyr Asp Gly Val Glu Asp Lys Arg Ile	
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Met Gly Met Gln Leu Asp Arg Ala Ser Ser Ser Leu Tyr Val Ala Phe	
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Ser Thr Cys Val Ile Lys Val Pro Leu Gly Arg Cys Glu Arg His Gly	
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Lys Cys Lys Lys Thr Cys Ile Ala Ser Arg Asp Pro Tyr Cys Gly Trp	
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Ile Lys Glu Gly Gly Ala Cys Ser His Leu Ser Pro Asn Ser Arg Leu	
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Thr Phe Glu Gln Asp Ile Glu Arg Gly Asn Thr Asp Gly Leu Gly Asp	
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Cys His Asn Ser Phe Val Ala Leu Asn Gly Val Ile Arg Glu Ser Tyr	
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Leu Lys Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala	
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Val Ile Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val	
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Tyr Cys Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg	
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Lys Glu Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val	
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Thr Lys Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Ile Lys	
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Lys Arg Glu Pro Ser Arg Gly Thr Arg Glu Trp Glu Arg Asn Gln Asn	
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Leu Ile Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val	
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Ile Pro Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser	
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Val Val Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val	
760 765 770 775	
gac caa cca aaa atg agc gag gtg gcc cag atg gcc ctg gag gag cag	2586
Asp Gln Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln	
780 785 790	
gag ggc att ctg gag tat aag aat atc aag gaa caa tta agt agt aag	2634
Ala Ala Thr Leu Glu Tyr Lys Thr Ile Lys Gln His Leu Ser Ser Lys	
795 800 805	
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Ser Pro Asn His Gly Val Asn Leu Val Gln Asn Leu Asp Ser Leu Pro	
810 815 820	
ccc aaa ctt cca caa cgg gag gcc tcc ctg ggt ccc cca aua gac tac	2730
Pro Lys Val Pro Gln Arg Gln Ala Ser Leu Gly Pro Pro Gly Ala Ser	
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 Leu Ser Ala Ile Gly Leu Ser Lys Arg Leu Glu Met His His Leu Ser
 840 845 850 855

tcc tac cgg att gat tat aag agg agc tac ccc aag aac tgg cta aag 2826
 Ser Tyr Gly Val Arg Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr
 860 865 870

aga agc cac ctg acc acc tac tct cat cag aag caa cac taaccacagac 2875
 Arg Ser His Leu Thr Thr Tyr Ser His Gln Lys Gln His
 875 880

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Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
 90 100 110

Asn Gly Thr Ser Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp	65	70	75	80
Ile Asp Thr Ser His Thr Val Glu Ile Tyr Cys Ser Lys Lys Leu Thr	85	90	95	
Trp Lys Ser Arg Glu Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys	100	105	110	
His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn	115	120	125	
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys	130	135	140	
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser	145	150	155	160
Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu	165	170	175	
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala	180	185	190	
Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg	195	200	205	
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln	210	215	220	
Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala	225	230	235	240
Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln	245	250	255	
Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln	260	265	270	
Trp Thr Ser Phe Ser Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp	275	280	285	
Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg	290	295	300	
Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn	305	310	315	320

Ser Ile Pro Gly Ser Ala Val Tyr Ala Tyr Asp Met Leu Asp Ile Ala
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Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
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Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
355 360 365

Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
370 375 380

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
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Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
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Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
435 440 445

Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
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Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
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Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
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515 520 525

Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
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Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
565 570 575

Gly Val Ile Arg Glu Ser Tyr Leu Lys Gly His Asp Gln Leu Val Pro
595 600 605

Val Thr Leu Leu Ala Ile Ala Val Ile Leu Ala Phe Val Met Gly Ala
605 610 615

Val Phe Ser Gly Ile Thr Val Tyr Cys Val Cys Asp His Arg Arg Lys
615 620 625

Asp Val Ala Val Val Gln Arg Lys Glu Lys Glu Leu Thr His Ser Arg
625 630 635 640

Arg Gly Ser Met Ser Ser Val Thr Lys Leu Ser Gly Leu Phe Gly Asp
645 650 655

Thr Gln Ser Lys Asp Pro Lys Pro Glu Ala Ile Leu Thr Pro Leu Met
660 665 670

His Asn Gly Lys Leu Ala Thr Pro Gly Asn Thr Ala Lys Met Leu Ile
675 680 685

Lys Ala Asp Gln His His Leu Asp Leu Thr Ala Leu Pro Thr Pro Glu
690 695 700

Ser Thr Pro Thr Leu Gln Gln Lys Arg Glu Pro Ser Arg Gly Thr Arg
705 710 715 720

Glu Trp Glu Arg Asn Gln Asn Leu Ile Asn Ala Cys Thr Lys Asp Met
725 730 735

Pro Pro Met Gly Ser Pro Val Ile Pro Thr Asp Leu Pro Leu Arg Ala
740 745 750

Ser Pro Ser His Ile Pro Ser Val Val Val Leu Pro Ile Thr Gln Gln
755 760 765

Gly Tyr Gln His Glu Tyr Val Asp Gln Pro Lys Met Ser Glu Val Ala
770 775 780

Gln Met Ala Leu Glu Asp Gln Ala Ala Thr Leu Glu Tyr Lys Thr Ile
785 790 795 800

Lys Glu His Leu Ser Ser Lys Ser Pro Asn His Gly Val Asn Leu Val
805 810 815

Glu Asn Leu Asp Ser Leu Pro Pro Lys Val Pro Gln Arg Glu Ala Ser
820 825 830

Leu Gly Pro Pro Gly Ala Ser Leu Ser Gln Thr Gly Leu Ser Lys Arg
835 840 845

Leu Glu Met His His Ser Ser Ser Tyr Gly Val Asn Tyr Lys Arg Ser
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Met Ile Met Asn Ile Ala Gln Ser Asn Ala Val
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Ile Ser Gln Trp Leu Phe Met Ile Arg Ser Phe His Cys Met Leu Thr
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Leu Phe Met Ser Lys Cys Asn Lys Cys Gln Asn Ile Asn Gln Lys Phe
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Leu Leu Gln Ile Ile Ala Lys Asn Leu Phe Ser Thr Phe Leu Leu Gln
45 50 55
tat tca aac aag tta agt gta att aac agt tta tta gta tta tta tta 362
Tyr Ser Lys Lys Phe Arg Val Ile Thr Arg Phe Gly Val Cys His Phe
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 Trp Ala Gln Arg Asp Phe Arg Phe Gln Arg Asn Lys Leu Cys Phe Thr
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ggt agt ggt ttt tgt cca tgt agt ttc agt gat ttt aga aat ttt agt 438
 Gly Ser Arg Cys Cys Pro Cys Arg Phe Arg Ala Phe Arg Asn Phe Arg
 95 100 105

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 Cys Asn Cys Ser Gly Thr Cys Gly Ser Phe Arg Phe Gly Ser Trp Arg
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 Phe Gly Pro Gly Ala Ser Phe Arg Cys Arg Arg Asp Arg Cys Ser Leu
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 Gln Phe Leu Arg Asn Lys Trp Cys Phe Thr Trp Ser Gln Cys Cys Pro
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ccagggagat ggtttagga ggtttagga ggtttagga ggtttagga ggtttagga 235

Met Lys Leu Leu Trp Gln Val

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Thr Val His His His Thr Trp Asn Ala Ile Leu Leu Pro Phe Val Tyr

10

15

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ctc acg ggc caa gtc tgg att ctg tgt gca gcc atc ggt ggt gcc ggc 335

Leu Thr Ala Gln Val Trp Ile Leu Cys Ala Ala Ile Ala Ala Ala Ala

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Phe Ser Lys Val Val Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln

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Gly Ile Pro Ser Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile

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cag atg atc cag gcc cac aat ttc cgc cac ctc cac cac ctg gag gtc 525

Gln Met Ile Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val

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95

100

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110

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aac ggc ctg gcc agt ctc agt aac ctg gag ctg ttc gac aac tgg atg 615

Asn Gly Leu Ala Ser Leu Ser Thr Leu His Leu Phe Asp Asn Trp Leu

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125

130

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aca gtc atc ctc agt ggt gtc ttc gaa tac ctg tcc aag ctg cgg gag 665

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145

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160

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Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu Phe Asn Leu Lys	
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Tyr Leu Asn Leu Gly Met Cys Asn Ile Lys Asp Met Pro Asn Leu Thr	
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Pro Leu Val Gly Leu Glu Glu Leu Glu Met Ser Gly Asn His Phe Pro	
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Glu Ile Arg Pro Gly Ser Phe His Gly Leu Ser Ser Leu Lys Lys Leu	
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ggg ctg gct tca ctt gtg gaa ctg aac ttg gcc cac aat aac ctg tct	1051
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His Leu His His Asn Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu	
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Ala Trp Trp Leu Arg Glu Tyr Ile Pro Thr Asn Ser Phe Cys Cys Gly	
315 320 325	
cgc tgt cat gct ccc atg cac atg cga ggc cgc tac ctc ctg gag gtg	1243
Arg Cys His Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val	
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gac cag gcc ccc ttc cag tgc tct gcc ccc ttc atc atg gac gca cct	1291
Asp Gln Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro	
345 350 355	

aga gac ctc aac att tct tct ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt	1339
Arg Asp Leu Asn Ile Ser Gln Gly Arg Met Ala Glu Leu Lys Cys Arg	
366 365 379 375	
act ecc cct atg tcc tcc gtg aag tgg atg ctc ccc aat ggg aca gtg	1387
Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr Val	
380 385 390	
ctc agc cac gcc tcc cgc cac cca agg aac tct gtc ctc aac gac ggc	1435
Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn Asp Gly	
395 400 405	
acc ttg aac ttt tcc cac gtg ctg ctt tca gac act ggg gtg tac aca	1483
Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly Val Tyr Thr	
410 415 420	
tgc atg ggg acc aat gtt gca ggc aac tcc aac gcc tgc gcc tac ctc	1531
Cys Met Gly Thr Asn Val Ala Gly Asn Ser Asn Ala Ser Ala Tyr Leu	
425 430 435	
aat ggg agc acg gct gag ctt aac acc tcc aac tac agc ttc ttc acc	1579
Asn Gly Ser Thr Ala Glu Leu Asn Thr Ser Asn Tyr Ser Phe Phe Thr	
440 445 450 455	
aca gga aca ggg gag acc acg gag atc tgc cct gag gac aca acg cga	1627
Thr Gly Thr Gly Glu Thr Thr Glu Ile Ser Pro Glu Asp Thr Thr Arg	
460 465 470	
aag tac aag cct gtt cct acc acg tcc act ggt tac cag ccg gca tat	1675
Lys Tyr Lys Pro Val Pro Thr Thr Thr Gly Tyr Gln Pro Ala Tyr	
475 480 485	
acc acc tct acc acg gtg ctc att cag act aac cgt gtg ecc aag cag	1723
Thr Thr Ser Thr Thr Val Leu Ile Gln Thr Thr Arg Val Pro Lys Gln	
490 495 500	
gtg gca gta ecc ggc aca gac acc act gac aag atg cag acc aat ctc	1771
Val Ala Val Pro Ala Thr Asp Thr Thr Arg Lys Met Gln Thr Ser Leu	
505 510 515	
gac gaa gca atg aag aac aac aag atc ctc att gac gac ttc gac gca	1819
Asp Glu Val Met Lys Thr Thr Lys Ile Ile Ile Gly Cys Phe Val Ala	
520 525 530 535	
gtg act ctg cta gct gcc gcc atg ttg aac gac ttc tat aac ctt cgt	1867
Val Thr Leu Leu Ala Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg	
540 545 550	

gag ggg cag cag cag ggg agt aca gtc aca gtc gtc ggg att gtt gag 1915
 Lys Arg His Gln Gln Arg Ser Thr Val Thr Ala Ala Arg Thr Val Glu
 555 560 565

ata att cag gtg gac gaa gac atc cca gca gca aca ttc gca gca gca 1963
 Ile Ile Gln Val Asp Glu Asp Ile Pro Ala Ala Thr Ser Ala Ala Ala
 570 575 580

aca gca gct ccc tcc ggt gta tca ggt gaa ggg gca gta gtg ctg ccc 2011
 Thr Ala Ala Pro Ser Gly Val Ser Gly Glu Gly Ala Val Val Leu Pro
 585 590 595

aca att cat gac cat att aac tac aac acc tac aaa cca gca cat ggg 2059
 Thr Ile His Asp His Ile Asn Tyr Asn Thr Tyr Lys Pro Ala His Gly
 600 605 610 615

gag cac tgg aca gaa aac agc ctg ggg aac tct ctg cac ccc aca gtc 2107
 Ala His Trp Thr Glu Asn Ser Leu Gly Asn Ser Leu His Pro Thr Val
 620 625 630

acc act atc tct gaa cct tat ata att cag acc cat acc aag gac aag 2155
 Thr Thr Ile Ser Glu Pro Tyr Ile Ile Gln Thr His Thr Lys Asp Lys
 635 640 645

gta cag gaa act caa ata tgactccct cccccaaaaa acttataaaa 2203
 Val Gln Glu Thr Gln Ile
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tgcgaatagaa tgcacacaaa gacagcaact ttgtacaga gtggggagag actttttctt 2263

gtatatgctt atatattaag tctatgggtt ggtaaaaaa aacagattat attaaaattt 2323

aaagacaaaa agtcaaaa 2341

0110-10

0110-117

0110-187

0113- Home captions

0120-10

Met Lys Leu Leu Trp Gln Val Thr Val His His His Thr Trp Asn Ala
 1 5 1 15

Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile Leu Cys
 20 25 30

Ala Ala Ile Ala Ala Ala Ala Ser Ala Gly Pro Gln Asn Cys Pro Ser

Val Cys Ser Tyr Ser Asn Gln Phe Ser Lys Val Val Cys Thr Arg Arg
55 60

Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser Asn Thr Arg Tyr Leu
65 70 75 80

Asn Leu Met Glu Asn Asn Ile Gln Met Ile Gln Ala Asp Thr Phe Arg
85 90 95

His Leu His His Leu Glu Val Leu Gln Leu Gly Arg Asn Ser Ile Arg
100 105 110

Gln Ile Gln Val Gly Ala Phe Asn Gly Leu Ala Ser Leu Ser Thr Leu
115 120 125

Glu Leu Phe Asp Asn Trp Leu Thr Val Ile Pro Ser Gly Ala Phe Glu
130 135 140

Tyr Leu Ser Lys Leu Arg Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu
145 150 155 160

Ser Ile Pro Ser Tyr Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu
165 170 175

Asp Leu Gly Glu Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe
180 185 190

Glu Gly Leu Phe Asn Leu Lys Tyr Leu Asn Leu Gly Met Cys Asn Ile
195 200 205

Lys Asp Met Pro Asn Leu Thr Pro Leu Val Gly Leu Glu Glu Leu Glu
210 215 220

Met Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly Ser Phe His Gly
225 230 235 240

Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser Glu Val Ser Leu
245 250 255

Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu Val Glu Leu Asn
260 265 270

Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp Leu Phe Thr Pro
275 280 285

Leu Arg Tyr Leu Val Glu Leu His Leu His His Asn Pro Trp Asn Cys

290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600			
Asp	Tyr	Arg	Leu	Leu	Trp	Leu	Ala	Trp	Trp	Leu	Arg	Gln	Tyr	Ile	Trp																			
305					310					315					320																			
Thr	Asn	Ser	Thr	Cys	Cys	Gly	Arg	Cys	His	Ala	Pro	Met	His	Met	Arg																			
				325					330					335																				
Gly	Arg	Tyr	Leu	Val	Glu	Val	Asp	Gln	Ala	Ser	Phe	Gln	Cys	Ser	Ala																			
				340				345					350																					
Pro	Phe	Ile	Met	Asp	Ala	Pro	Arg	Asp	Leu	Asn	Ile	Ser	Glu	Gly	Arg																			
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Met	Ala	Gln	Leu	Lys	Cys	Arg	Thr	Pro	Pro	Met	Ser	Ser	Val	Lys	Trp																			
				370			375				380																							
Leu	Leu	Pro	Asn	Gly	Thr	Val	Leu	Ser	His	Ala	Ser	Arg	His	Pro	Arg																			
385					390				395					400																				
Ile	Ser	Val	Leu	Asn	Asp	Gly	Thr	Leu	Asn	Phe	Ser	His	Val	Leu	Leu																			
				405				410					415																					
Ser	Asp	Thr	Gly	Val	Tyr	Thr	Cys	Met	Gly	Thr	Asn	Val	Ala	Gly	Asn																			
				420				425				430																						
Ser	Asn	Ala	Ser	Ala	Tyr	Leu	Asn	Gly	Ser	Thr	Ala	Glu	Leu	Asn	Thr																			
				435			440				445																							
Ser	Asn	Tyr	Ser	Phe	Phe	Thr	Thr	Gly	Thr	Gly	Glu	Thr	Thr	Glu	Ile																			
				450			455				460																							
Ser	Pro	Glu	Asp	Thr	Thr	Arg	Lys	Tyr	Lys	Pro	Val	Pro	Thr	Thr	Ser																			
465					470				475				480																					
Thr	Gly	Tyr	Gln	Pro	Ala	Tyr	Thr	Thr	Ser	Thr	Thr	Val	Leu	Ile	Gln																			
				485				490				495																						
Thr	Thr	Arg	Val	Pro	Lys	Gln	Val	Ala	Val	Pro	Ala	Thr	Asp	Thr	Thr																			
				500				505				510																						
Asp	Lys	Met	Gln	Thr	Ser	Leu	Asp	Glu	Val	Met	Lys	Thr	Thr	Lys	Ile																			
				515			520				525																							
Ile	Ile	Gly	Cys	Phe	Val	Ala	Val	Thr	Leu	Leu	Ala	Ala	Ala	Met	Leu																			
530					535				540																									
Ile	Val	Phe	Tyr	Lys	Leu	Arg	Lys	Arg	His	Gln	Gln	Arg	Ser	Thr	Val																			

545

550

555

560

Thr Ala Ala Arg Thr Val Glu Ile Ile Gln Val Asp Glu Asp Ile Pro
565 570 575

Ala Ala Thr Ser Ala Ala Ala Thr Ala Ala Pro Ser Gly Val Ser Gly
580 585 590

Glu Gly Ala Val Val Leu Pro Thr Ile His Asp His Ile Asn Tyr Asn
595 600 605

Thr Tyr Lys Pro Ala His Gly Ala His Trp Thr Glu Asn Ser Leu Gly
610 615 620

Asn Ser Leu His Pro Thr Val Thr Thr Ile Ser Glu Pro Tyr Ile Ile
625 630 635 640

Gln Thr His Thr Lys Asp Lys Val Gln Glu Thr Gln Ile
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agaggagctc ctagctcact taagccgggg taaggatgtt tctcttttc gagcagaat 180

ccaggagat agtgattat gaagtgcca caac atg aag ctg tgg tgg aag gta 240

Met Lys Leu Leu Trp Gln Val

1

5

act ggg caa caa caa aat tgg aat aac atc ctg ctg ccc tta gta taa 300

Thr Val His His His Thr Trp Asn Ala Ile Leu Leu Pro Phe Val Tyr

10

15

20

tgc aag ggg caa ggg tgg aat ctg tgt gca gcc aac gct gct gcc gcc 360

Leu Thr Ala Gln Val Trp Ile Leu Cys Ala Ala Ile Ala Ala Ala Ala

25	30	35	
taa gta ggg aac cag aat ttt ctt ttt gtc tgc tgg tgc aat aac cag	379		
Ser Ala Gly Pro Gln Asn Cys Pro Ser Val Cys Ser Cys Ser Asn Gln			
40 45 50 55			
ttt agc aag gta gta tta aag cgt ggt ggc atc ttc gag gtc ccg cag	427		
Phe Ser Lys Val Val Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln			
60 65 70			
ggc att ccc tgc aac aac cgg tac ctc aac ctc atg gag aac aac atc	475		
Gly Ile Pro Ser Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile			
75 80 85			
cag atg atc cag gcc gat aac ttc cgc cac ctc cac cac ctg gag gtc	523		
Gln Met Ile Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val			
90 95 100			
ctg cag ttg ggc agg aac tcc atc cgg cag att gag gtg ggg gcc ttc	571		
Leu Gln Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe			
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aac gcc ctg gcc agc ctc agc aac ctg gag ctg ttc gac aac tgg ctg	619		
Asn Gly Leu Ala Ser Leu Ser Thr Leu Glu Leu Phe Asp Asn Trp Leu			
120 125 130 135			
aca gtc atc cct agc ggg gcc ttt gaa tac ctg tcc aag ctg cgg gag	667		
Thr Val Ile Pro Ser Gly Ala Phe Gln Tyr Leu Ser Lys Leu Arg Glu			
140 145 150			
ctc tgg ctt cgc aac aac ccc atc gaa agc atc ccc tct tac gcc ttc	715		
Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr Ala Phe			
155 160 165			
aac cgg gtg ccc tcc ctc atg cgc ctg gac ttg ggg gag ttc aag aag	763		
Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu Leu Lys Lys			
170 175 180			
ctg gag tat atc tct gaa gga gta tta ggg gta ctg ttc aac ctc aag	811		
Leu Glu Tyr Ile Ser Gln Gly Ala Phe Gln Gly Leu Phe Asn Leu Lys			
185 190 195			
tat ctc aac tta ggc att tga aac att aaa gac atg cct aat ctc aac	859		
Tyr Leu Asn Leu Gly Met Cys Asn Ile Lys Asp Met Pro Asn Leu Thr			
200 205 210 215			
aac ctg gta gta ctg gag gag ctg gag atg tta gta aac aac ttc cct	907		
Pro Leu Val Gly Leu Glu Glu Leu Gln Met Ser Gly Asn His Phe Pro			

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gag atc agg cct ggc tcc ttc cat ggc cta ggc ttc cta aag aag cta	945		
Glu Ile Arg Pro Gly Ser Phe His Gly Leu Ser Ser Leu Lys Lys Leu			
235	240	245	
tgg gtc atg aac tca cag gtc agc ctg att gag cgg aat gct ttt gac	1003		
Trp Val Met Asn Ser Gln Val Ser Leu Ile Glu Arg Asn Ala Phe Asp			
250	255	260	
ggg ctg gct tca ctt gtg gaa ctc aac ttg gcc cac aat aac ctc tct	1051		
Gly Leu Ala Ser Leu Val Glu Leu Asn Leu Ala His Asn Asn Leu Ser			
265	270	275	
tct ttg ccc cat gac ctc ttt acc ccg ctg agg tac ctg gtg gag ttg	1099		
Ser Leu Pro His Asp Leu Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu			
280	285	290	295
cat cta cac cac aac cct tgg aac tgt gat tgt gac att ctg tgg cta	1147		
His Leu His His Asn Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu			
300	305	310	
gcc tgg tgg ctt cga gag tat ata ccc acc aat tct acc tgc tgt gcc	1195		
Ala Trp Trp Leu Arg Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly			
315	320	325	
cgc tgt cat gct ccc atg cac atg cga gcc cgc tac ctc gtg gag gtg	1243		
Arg Cys His Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val			
330	335	340	
gac cag gcc tcc ttc cag tgc tct gcc ccc ttc atc atg gac gca cct	1291		
Asp Gln Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro			
345	350	355	
cga gac ctc aac att tct gag ggt cgg atc cca gaa ctt aag tgt cgg	1339		
Arg Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg			
360	365	370	375
act acc cct atg tcc tcc gtc aag tgg ttc ctg ccc aat ggc acc gtc	1387		
Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr Val			
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ctc agc cac gcc tcc cgc cac cca agg atc tct gtc ctc aac gac gcc	1435		
Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn Asp Gly			
395	400	405	
acc ttg aac ttt tcc cac gtg ctg ctt ttc gac acc ggg gtg tac aca	1483		
Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly Val Tyr Thr			

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Tyr Met Gly Thr Asn Val Ala Gly Asn Ser Asn Ala Ser Ala Tyr Leu			
425	430	435	
aat ggg agt aag gct gag ctt aac aac tcc aac tat agt ttc ttc acc	1579		
Asn Gly Ser Thr Ala Glu Leu Asn Thr Ser Asn Tyr Ser Phe Phe Thr			
440	445	450	455
aca gga aca ggg gag acc acg gag atc tgg cct gag gac aca acg cga	1627		
Thr Gly Thr Gly Glu Thr Thr Glu Ile Ser Pro Glu Asp Thr Thr Arg			
	460	465	470
aag tac aag cct gtt cct acc acg tcc act ggt tac cag ccg gca tat	1675		
Lys Tyr Lys Pro Val Pro Thr Thr Ser Thr Gly Tyr Gln Pro Ala Tyr			
	475	480	485
acc acc tct acc acg gtg ctc att cag act acc cgt gtg ccc aag cag	1723		
Thr Thr Ser Thr Thr Val Leu Ile Gln Thr Thr Arg Val Pro Lys Gln			
	490	495	500
gtg gca gta ccc gcg aca gac acc act gac aag atg cag acc agc ctg	1771		
Val Ala Val Pro Ala Thr Asp Thr Thr Asp Lys Met Gln Thr Ser Leu			
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gat gaa gtc atg aag acc acc aag atc atc att ggt tgc ttt gtg gca	1819		
Asp Gln Val Met Lys Thr Thr Lys Ile Ile Ile Gly Cys Phe Val Ala			
	520	525	530
gtg act ctg ata gct gcc gcc atg ttg att gtc ttc tat aaa ctt cgt	1867		
Val Thr Leu Leu Ala Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg			
	540	545	550
agc atg car cag cag cgg agt aca gtc aca acc gac ccc aca atg gag	1915		
Lys Arg His Gln Gln Arg Ser Thr Val Thr Ala Ala Pro Thr Leu Glu			
	555	560	565
aga aac cac agg gac aaa aac aca cca caa caa aac cac cca aca caa	1963		
Arg Lys His Arg Asp Lys Asn Thr Pro Gln Gln Lys His Pro Gln Gln			
	570	575	580
aaa aaa caa ttc ttc cca gta aaacattaaa ggcacata ggcacata	2014		
Lys Gln Gln Pro Pro Pro Val			
	585	590	
aaacacacac acataaaaaa caaaacacac acaaacacac aatagggggc caatggacag	2074		

aaaaatggtt ggggaactct gtgacaccca cagtcacaaa tatatctgaa tttatattaa 2134
 ttatgagaaa taaagagaa aggttatagg aaacttcaat atgactttaa tttacaaa 2144
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Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile Leu Cys

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Ala Ala Ile Ala Ala Ala Ala Ser Ala Gly Pro Gln Asn Cys Pro Ser

35 40 45

Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val Cys Thr Arg Arg

50 55 60

Gly Leu Leu Ile Val His Gln Gly Ile Leu Ser Asn Thr Val Lys Leu

65 70 75 80

Asn Leu Ser Glu Asn Asn Ile Gln Met Ile Gln Ala Asp Thr Phe Arg

85 90 95

His Leu His His Leu Gln Val Leu Gln Leu Gly Arg Asn Ser Ile Arg

100 105 110

Gln Ile Gln Val Gly Ala Phe Asn Gly Leu Ala Ser Leu Ser Thr Leu

115 120 125

Glu Leu Ile Arg Asn Trp Leu Thr Val Ile Pro Ser Gly Ala Ile Glu
130 135 140

Tyr Leu Ser Lys Leu Arg Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu
145 150 155 160

Ser Ile Pro Ser Tyr Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu
165 170 175

Asp Leu Gly Glu Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe
180 185 190

Glu Gly Leu Phe Asn Leu Lys Tyr Leu Asn Leu Gly Met Cys Asn Ile
195 200 205

Lys Asp Met Pro Asn Leu Thr Pro Leu Val Gly Leu Glu Glu Leu Glu
210 215 220

Met Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly Ser Phe His Gly
225 230 235 240

Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser Gln Val Ser Leu
245 250 255

Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu Val Glu Leu Asn
260 265 270

Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp Leu Phe Thr Pro
275 280 285

Leu Arg Tyr Leu Val Glu Leu His Leu His His Asn Pro Trp Asn Cys
290 295 300

Asp Cys Asp Ile Leu Trp Leu Ala Trp Trp Leu Arg Glu Tyr Ile Pro
305 310 315 320

Thr Asn Ser Thr Cys Cys Gly Arg Cys His Ala Pro Met His Met Arg
325 330 335

Gly Arg Tyr Leu Val Glu Val Asp Gln Ala Ser Phe Gln Cys Ser Ala
340 345 350

Pro Phe Ile Met Asp Ala Pro Arg Asp Leu Asn Ile Ser Glu Gly Arg
355 360 365

Met Ala Glu Leu Lys Cys Arg Thr Pro Pro Met Ser Ser Val Lys Trp
370 375 380

Leu Leu Pro Asn Gly Thr Val Leu Ser His Ala Ser Arg His Pro Arg
385 395 405

Ile Ser Val Leu Asn Asp Gly Thr Leu Asn Phe Ser His Val Leu Leu
405 410 415

Ser Asp Thr Gly Val Tyr Thr Cys Met Gly Thr Asn Val Ala Gly Asn
420 425 430

Ser Asn Ala Ser Ala Tyr Leu Asn Gly Ser Thr Ala Glu Leu Asn Thr
435 440 445

Ser Asn Tyr Ser Phe Phe Thr Thr Gly Thr Gly Glu Thr Thr Glu Ile
450 455 460

Ser Pro Glu Asp Thr Thr Arg Lys Tyr Lys Pro Val Pro Thr Thr Ser
465 470 475 480

Thr Gly Tyr Gln Pro Ala Tyr Thr Thr Ser Thr Thr Val Leu Ile Gln
485 490 495

Thr Thr Arg Val Pro Lys Gln Val Ala Val Pro Ala Thr Asp Thr Thr
500 505 510

Asp Lys Met Gln Thr Ser Leu Asp Glu Val Met Lys Thr Thr Lys Ile
515 520 525

Ile Ile Gly Cys Phe Val Ala Val Thr Leu Leu Ala Ala Ala Met Leu
530 535 540

Ile Val Phe Tyr Lys Leu Arg Lys Arg His Gln Gln Arg Ser Thr Val
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Thr Ala Ala Pro Thr Leu Glu Arg Lys His Arg Asp Lys Asn Thr Pro
565 570 575

Gln Gln Lys His Pro Gln Thr Lys Gln Gln His His His Val
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<213> Homo sapiens

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<222> (421)..(1287)

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accgtttcag cctgggcagc cctctgggac ccgaggttgg accctactgt gacacaccta 180

ccatgcccgc actcttcaac ctctcttggc ttgccttggc ctgcagccct gttcacacta 240

cctgtcaaaa gtcagatgac aaaaaagcgc ctcaaaagac gctgctggag aagagtcagt 300

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tggttcttga gcctgcagc tactgctcgg caaagcccg ggacagacac ttgctcggg 420

atg tac tgg gct atg tca ctc cac cag tgg aac agc cat ggc tac gat 468
Met Tyr Trp Ala Met Ser Leu His Gln Trp Asn Ser His Gly Tyr Asp
1 5 10 15

gtc acc aag gtc ttt ggg agc aag ttc aca cag atc tca ccc gtc tgg 516
Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp
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Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu
35 40 45

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His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys
50 55 60

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Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asn Trp Thr Tyr Asp
65 70 75 80

gat ttc tgg aac gtc tta gag agc gag gat gag ata gag gag ctg agc 708
Asp Phe Arg Asn Val Leu Asp Ser His Asp Glu Ile Glu Glu Leu Ser
85 90 95

aag acc gtg gtc cag gtg gta aag aac cag cat tta gat ggc tta ggc 756

Lys Thr Val Val Gln Val Ala Lys Asn Gln His His Asp Gly Phe Val	
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gtg gag gtc tgg aac cag ctg cta agt cag aag tgg gtg ggc ctc atc	894
Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile	
115 120 125	
cac atg ctc acc cac ttg gcc gag gct ctg cac cag gcc cgg ctg ctg	852
His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu	
130 135 140	
gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg acc gac cag ctg	900
Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu	
145 150 155 160	
ggc atg ttc acg cac aag gag ttt gag cag ctg gcc ccc gtg ctg gat	948
Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp	
165 170 175	
ggt ttc agc ctc atg acc tac gac tac tct aca gcg cat cag cct ggc	996
Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly	
180 185 190	
cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc cag gtc ctg gac	1044
Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp	
195 200 205	
cag aag ttc aag tgg cga agc aaa atc ctc ctg ggg ctc aac ttc tat	1092
Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr	
210 215 220	
ggt atg gac tac gcg acc tcc aag gat gcc cgt gag cct gtt gtc ggg	1140
Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly	
225 230 235 240	
gcc agg tac atg cag aca ctg aag tct gca ttc gta ctc tta gca aac	1188
Ala Arg Tyr Met Gln Thr Leu Lys Ser Ala Phe Val Leu Leu Ala Asn	
245 250 255	
tty gaa aat ttg agg tga aat ttt tca att aat aaa aat aaa aat aaa	1236
Leu Glu Asn Leu Arg Arg Asn Ser Ser Asn Lys Lys Lys Lys Lys Lys	
260 265 270	
aat ttt ttc tgt ttc ttc tct tct gtc ttc tgg ttt gga gac aac aaa	1284
Asn Phe Phe Cys Phe Phe Ser Ser Val His Ser Phe Gly Asp His Lys	
275 280 285	
cac tagatccatt gaatttgtcc cacagctcac gaataacacat tttaacctttt gga	1340

His

<210> 14

<211> 289

<212> FRT

<213> Homo sapiens

<400> 14

Met Tyr Trp Ala Met Ser Leu His Gln Trp Asn Ser His Gly Tyr Asp
1 5 10 15

Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp
20 25 30

Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu
35 40 45

His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys
50 55 60

Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp
65 70 75 80

Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser
85 90 95

Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val
100 105 110

Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile
115 120 125

His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu
130 135 140

Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu
145 150 155 160

Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp
165 170 175

Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly
180 185 190

Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp
195 200 205

Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr
 210 215 220

Gly Met Arg Tyr Ala Thr Ser Lys Asp Ala Arg Glu Phe Val Val Gly
 225 230 235 240

Ala Arg Tyr Met Gln Thr Leu Lys Ser Ala Phe Val Leu Leu Ala Asn
 245 250 255

Leu Glu Asn Leu Arg Arg Asn Ser Ser Asn Lys Lys Lys Lys Lys Lys
 260 265 270

Asn Phe Phe Cys Phe Phe Ser Ser Val Phe Ser Phe Gly Asp His Lys
 275 280 285

His

(210): 15
 (211): 1426
 (212): BHA
 (213): Homo sapiens

(220):
 (221): CNS
 (222): (96)11 (905)

(400): 15
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tgcgcgggcr gcgcgcggat ttgctttctc agaag atg cac tat tat aga tac 113
 Met His Tyr Tyr Arg Tyr
 1 5

tat aac gta aag gta agt tgc tgg tac aag tgc ctc ctc ttc tgc tgc 161
 Ser Asn Ala Lys Val Ser Cys Trp Tyr Lys Tyr Leu Leu Ile Ser Tyr
 1 15 21

aac atc atc ttc tgg tgg gtt gga gtt ttc ttc ctc gga ttc tgc tgc 219
 Asn Ile Ile Ile Trp Leu Ala Gly Val Val Phe Leu Gly Val Gly Leu
 25 30 35

tgg gca tgc agt gaa aag ggt gtc ctg tcc aac ctc aac aia gtc aac 257
 Trp Ala Trp Ser Glu Lys Gly Val Leu Ser Asp Leu Thr Lys Val Thr
 40 45 50

agg atg atg gga atg gat atg gag ggt ctg gtc ctg atg atg ggt gat	395
Arg Met His Gly His Asp Pro Ala Val Leu Val Leu Met Val Gly Ala	
55 60 65 70	
gtg atg ttc atc ctg ggt ttc gcc ggc cgt gtc ggg ggc cgt agt gag	398
Val Met Phe Thr Leu Gly Phe Ala Gly Arg Val Gly Ala Arg Arg Glu	
75 80 85	
aat atc cgt ctg ctc aac ttt ttc tgt gcc acc atc gtg ctc atc ttc	401
Asn Ile Cys Leu Leu Asn Phe Phe Cys Gly Thr Ile Val Leu Ile Phe	
90 95 100	
ttc ctg gag ctg gct gtc gcc gtc ctg gcc ttc ctg ttc cag gac tgg	449
Phe Leu Glu Leu Ala Val Ala Val Leu Ala Phe Leu Phe Gln Asp Trp	
105 110 115	
gtg agg gac agt ttc cgt gag ttc ttc gag agc aac atc aag tcc tac	497
Val Arg Asp Arg Phe Arg Glu Phe Phe Glu Ser Asn Ile Lys Ser Tyr	
120 125 130	
cgg gac gat atc gat ctg caa aac ctc atc gac tcc ctt cag aaa gct	545
Arg Asp Asp Ile Asp Leu Gln Asn Leu Ile Asp Ser Leu Gln Lys Ala	
135 140 145 150	
aac cag tgc tgt gcc gca tat gcc cct gaa gac tgg gac ctc aac gtc	593
Asn Gln Cys Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val	
155 160 165	
tac ttc aat tgc agc ggt gcc agc tac agc cga gag aag tgc ggg gtc	641
Tyr Phe Asn Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val	
170 175 180	
ccc ttc tcc tgc tgc gtc cca gat cct gcc caa aaa gtt gtc aac aca	689
Pro Phe Ser Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr	
185 190 195	
cag tgt gga tat gat gtc agt atc cag ctg aag agc aag tgg gat gat	737
Gln Tyr Gly Tyr Asp Val Arg Ile Val Leu Lys Ser Lys Trp Asp Glu	
200 205 210	
tac atc ttc atc aaa ggt tat atc agt atg ctg gaa agc tgg ctg atc	785
Ser Ile Ile Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro	
215 220 225 230	
cgg aac att tac att gtc gct gcc gtc ttc atc gcc atc tgc ctg ttc	833
Arg Asn Ile Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu	
235 240 245	

caa ata ttt ggc atc ttc cta tta agg aag atg atc taa gac atc aag 841
 Gln Ile Phe Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Gln
 250 255 260

gca gtg aag aac ggc cat caa ttc tgaggagcag agttgaggga gccgaggtga 941
 Ala Val Lys Thr Gly His His Phe
 265 270

gccacgctgg gaggccagag ccttctcttg ccacacagccc taagtcacaga gggagaggag 991
 ccgacacccc cagagccagt gcccatcttt aagcatcagc gtgacgtgac ctctctgttt 1055
 ctgcttgctg gtgctgaaga ccaagggctc ccttgatac ctgcccaaac ttgtgactgc 1115
 atccctctgg agtctaccca qagacagaga atgtgtcttt atgtgggagt ggtgactctg 1175
 aaagacagag agggctctctg tggctgacag gagggcttga ctacagacccc ctgcagctca 1235
 agcatgtctg caggacaccc tggcctctc tccactggca tccagacatc tgcttggggt 1295
 catccacatc tgtgggtggg ccgtgggtag agggaccac aggcgtggac agggcatctc 1355
 cctccatcaa gcaaaagcagc atgttggtct gccctgaacg ggaggcggac gtggcccccg 1415
 tgggcctctc cga 1428

<210> 16
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met His Tyr Tyr Arg Tyr Ser Asn Ala Lys Val Ser Cys Trp Tyr Lys
 1 5 10 15
 Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly Val Val
 20 25 30
 Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val Leu Ser
 35 40 45
 Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Ala Val Leu
 50 55 60
 Val Leu Met Val Gly Ala Val Met Phe Thr Leu Gly Phe Ala Gly Arg
 65 70 75 80

Val Gly Ala Arg Arg Glu Asn Ile Cys Leu Leu Asn Phe Phe Cys Gly	85	90	95
Thr Ile Val Leu Ile Phe Phe Leu Gln Leu Ala Val Ala Val Leu Ala	100	105	110
Phe Leu Phe Gln Asp Trp Val Arg Asp Arg Phe Arg Glu Phe Phe Glu	115	120	125
Ser Asn Ile Lys Ser Tyr Arg Asp Asp Ile Asp Leu Gln Asn Leu Ile	130	135	140
Asp Ser Leu Gln Lys Ala Asn Gln Cys Cys Gly Ala Tyr Gly Pro Glu	145	150	155
Asp Trp Asp Leu Asn Val Tyr Phe Asn Cys Ser Gly Ala Ser Tyr Ser	165	170	175
Arg Glu Lys Cys Gly Val Pro Phe Ser Cys Cys Val Pro Asp Pro Ala	180	185	190
Gln Lys Val Val Asn Thr Gln Cys Gly Tyr Asp Val Arg Ile Gln Leu	195	200	205
Lys Ser Lys Trp Asp Glu Ser Ile Phe Thr Lys Gly Cys Ile Gln Ala	210	215	220
Leu Glu Ser Trp Leu Pro Arg Asn Ile Tyr Ile Val Ala Gly Val Phe	225	230	235
Ile Ala Ile Ser Leu Leu Gln Ile Phe Gly Ile Phe Leu Ala Arg Thr	245	250	255
Leu Ile Ser Asp Ile Glu Ala Val Lys Thr Gly His His Phe	260	265	270

<210> 17

<211> 17

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> [51,...(983)]

<230> 17

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Met Ser	
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aat ccc agc ggc cca cca cca tat gaa gac att aac ccc atg tac cca	104
Asn Pro Ser Ala Pro Pro Pro Tyr Glu Asp Asn Asn Pro Leu Tyr Pro	
5 10 15	
ggc cct atg ccc cct ggc ggc tat ggc cag cca cct gtc ctg cca gga	152
Gly Pro Leu Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu Pro Gly	
20 25 30	
ggg tat cct ggc tac cct ggc tac ccc cag cct ggc tac ggt cac cct	200
Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr Gly His Pro	
35 40 45 50	
gct ggc tac cca cag ccc atg ccc ccc acc cac ccc atg ccc atg aac	248
Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro Met Asn	
55 60 65	
tac ggc cca ggc cat ggc tat gat ggc gag gag aga ggc gtg agt gat	296
Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val Ser Asp	
70 75 80	
agc ttc ggc cct gga gaa tgg gat gac cgg aaa gtg cga cac act ttt	344
Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His Thr Phe	
85 90 95	
atc cga aag gti tac tcc atc atc tcc ggc cag ctg ctg atc act ggc	392
Ile Arg Lys Val Tyr Ser Ile Ile Ser Gly Gln Leu Leu Ile Thr Gly	
100 105 110	
ggc atc att gct atc ttc acc ttt ggc gaa cct gtc agc gcc ttt ggc	440
Ala Ile Ile Ala Ile Phe Thr Phe Gly Glu Pro Val Ser Ala Phe Gly	
115 120 125 130	
agg aga aat gtg gat gtc tac tac gtc att att gat gtc att agt gtc	488
Arg Arg Asn Val Ala Val Tyr Tyr Val Ala Tyr Ala Val Phe Ser Val	
135 140 145	
acc tac ctg atc cct ggc tgc tgc cag gga att aga ccc cct ttc cca	536
Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg Ile Pro	
150 155 160	
agg aac atc att ctg ctg acc cct ttt act ttt ggc atg ggc ttc atg	584
Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly Phe Met	
165 170 175	

atg ggt aat att tcc agt atg tac gaa acc aat ttt ttt att gaa 651
 Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile Ile Ala
 180 185 190

atg att att att ggg ggg gta tcc att tcc gta acc att ttt ttt 656
 Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe Cys Phe
 195 200 205 210

cag acc aag gtg gac ttc acc tgg tgc aca ggc ctc ttc tgt gtc ctg 728
 Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys Val Leu
 215 220 225

gga att gtg ctc ctg gtg act ggg att gtc act agc att gtg ctc tac 776
 Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val Leu Tyr
 230 235 240

ttc caa tac gtt tac tgg ctc cac atg ctc tat gct gct ctg ggg gcc 824
 Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu Gly Ala
 245 250 255

att tgt ttc acc ctg ttc ctg gct tac gac aca cag ctg gtc ctg ggg 872
 Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val Leu Gly
 260 265 270

aac cgg aag cac acc atc agt ccc gag gac tac atc act ggc gcc ctg 920
 Asn Arg Lys His Thr Ile Ser Pro Glu Asp Tyr Ile Thr Gly Ala Leu
 275 280 285 290

cag att tac aca gac atc atc tac atc ttc acc ttt gta ctg cag ctg 958
 Gln Ile Tyr Thr Asp Ile Ile Tyr Ile Phe Thr Phe Val Leu Gln Leu
 295 300 305

atg ggg gat cgc aat taaggagcaa gcccacattt tcaacagatc ctgggcctc 1023
 Met Gly Asp Arg Asn
 310

ccttcacagg taaggggtg ggcctatga ctggggctg ggtttggg cttttctt 1073

ccttcaggt taacagccaa gtttccttct tttctggg aagggggc tttctggata 1143

tttcttctt ggttttgtt ggggaagg ggttaagg ttaatttt ctctgggtt 1193

gtttcaggg gactaggctg aagatgtgtc ttctccggc cactactgt atgaacac 1263

attcttcta acagctgggg ttgtgaggaa tatgaaga gtttttga tggtagaag 1323

ggaatatgaa aggtagaagt gaattcaagg taaggaggtt cttctccaa ctcttcaca 1383

42

Ser Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg
 145 150 155 160

Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly
 165 170 175

Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile
 180 185 190

Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe
 195 200 205

Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys
 210 215 220

Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val
 225 230 235 240

Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu
 245 250 255

Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val
 260 265 270

Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu Asp Tyr Ile Thr Gly
 275 280 285

Ala Leu Gln Ile Tyr Thr Asp Ile Ile Tyr Ile Phe Thr Phe Val Leu
 290 295 300

Gln Leu Met Gly Asp Arg Asn
 305 310

<210> 1:
 <211> 1686
 <212> 116
 <213> Homo sapiens

<220>
 <221> CIG
 <222> (372)...(1277)

<223>
 <221> misc feature
 <222> (117)...(167)
 <223> an n may be any one of a or t or g or c

<400> 10

ttcataaaca aaatcagggc cagggcaggt ggctcatttt taaagtcac aagaaaaat 60

agtaattaaa aaatagaaaa ataaatat gtacaccaaa ataatgtaga aaatggaac 120

taagaaataa tatttgaaa taatataaaa tgaagctaca gaaggcataa gtaagtcac 180

atgttggttc ttgaaagac tattaaataa ttacacagaa agtctaataa agagaaaaga 240

gagaaaaaaa ctgtcagaa gtacccgaac tgtactgctt ctacagttag aacacggatc 300

tgacttgctg gcagcccaag tgtgacaagt gcaatgctgc ctatcctcac ctggctcacc 360

tgccatctgc c atg gca gac tca tcc ttc cgg ttt cct cgc aca tgg tgg 420

Met Ala Asp Ser Ser Phe Arg Phe Pro Arg Thr Trp Trp

1

5

10

cag tct gcg gag gat gtg cac aga gaa aag atc cag tta gac ctg gaa 480

Gln Ser Ala Glu Asp Val His Arg Glu Lys Ile Gln Leu Asp Leu Glu

15

20

25

gct gaa ttc tac ttc act cac cta att gtg atg ttc aag tcc ccc agg 540

Ala Glu Phe Tyr Phe Thr His Leu Ile Val Met Phe Lys Ser Pro Arg

30

35

40

45

ccg gct gcc atg gtg ctg gac cgc tcc cag gac ttt ggg aaa aca tgg 600

Pro Ala Ala Met Val Leu Asp Arg Ser Gln Asp Phe Gly Lys Thr Trp

50

55

60

aag cct tat aag tac ttt gcg act aac tgc tcc gct aca ttt ggc ctg 660

Lys Pro Tyr Lys Tyr Phe Ala Thr Asn Cys Ser Ala Thr Phe Gly Leu

65

70

75

gaa gat gat gtt gtc aag aag ggc gct att tgt act tct aaa tac tcc 720

Glu Asp Asp Val Val Lys Lys Gly Ala Ile Cys Thr Ser Lys Tyr Ser

80

85

90

agt cct ttt cca tgc act ggc ggc gag gtt att ttc aaa gat ttg tca 780

Ser Pro Phe Pro Cys Thr Gly Gly Glu Val Ile Phe Lys Ala Leu Ser

95

100

105

cca cca tac gat aca gag aac att tac agt gct aaa gtt cag gag cag 840

Pro Pro Tyr Asp Thr Glu Asn Pro Tyr Ser Ala Lys Val Gln Glu Gln

110

115

120

125

ctg aag atc aac aac att tgg gtg cag ctg ctg aaa cca cag tct tgt 900

Leu Lys Ile Thr Asn Leu Arg Val Gln Leu Leu Lys Arg Gln Ser Cys

130	135	140	
ccg tgt cag aga tat gac cag acg gaa gag cct cca cat ttt aca cac	842		
Pro Cys Gln Arg Asn Asp Leu Asn Gln Gln Pro Gln His Phe Thr His			
145	150	155	
tat gca atc tat gat ttc att gtc aag ggc agc tgc ttc tgc aat ggc	890		
Tyr Ala Ile Tyr Asp Phe Ile Val Lys Gly Ser Cys Phe Cys Asn Gly			
160	165	170	
cac gct gat caa tgc ata cct gtt cat ggc ttc aga cct gtc aag gcc	938		
His Ala Asp Gln Cys Ile Pro Val His Gly Phe Arg Pro Val Lys Ala			
175	180	185	
cca gga aca ttc cac atg gtc cat ggg aag tgt atg tgt aag cac aac	986		
Pro Gly Thr Phe His Met Val His Gly Lys Cys Met Cys Lys His Asn			
190	195	200	205
aca gca ggc agc cac tgc cag cac tgt gcc ccg tta tac aat gac cgg	1034		
Thr Ala Gly Ser His Cys Gln His Cys Ala Pro Leu Tyr Asn Asp Arg			
210	215	220	
cca tgg gag gca gct gat ggc aaa acg ggg gct ccc aac gag tgc aga	1082		
Pro Trp Glu Ala Ala Asp Gly Lys Thr Gly Ala Pro Asn Glu Cys Arg			
225	230	235	
acc tgc aag tgt aat ggg cat gct gat acc tgt cac ttc gac gtt aat	1130		
Thr Cys Lys Cys Asn Gly His Ala Asp Thr Cys His Phe Asp Val Asn			
240	245	250	
gtg tgg gag gca tca ggg aat cgt agt ggt ggt gtc tgt gat gac tgt	1178		
Val Trp Glu Ala Ser Gly Asn Arg Ser Gly Gly Val Cys Asp Asp Cys			
255	260	265	
cag cac aac aca gaa gga cag cat tgc cag agg tgc aag cca gga ttc	1226		
Gln His Asn Thr Glu Gly Gln Tyr Cys Gln Arg Cys Lys Pro Gly Phe			
270	275	280	
tat cgt cag ctg cgg aga ccc ttc tca ggt cca gat ggt tgc aca cgt	1274		
Tyr Arg Arg Leu Arg Arg Pro Phe Ser Ala Pro Asp Ala Cys Lys Arg			
285	290	300	
aag taacttggtg ttctcagaaa ataggctgat ttgtataaga gatgaatctc	1327		
Lys			
tttatccctc attctgctaa cccaagagaa ggaggtcatt gaggttctga gataacacac	1387		
tttcagatat cgggttaattt cttcattgat aagaagcaag aattcttcac ccttgggtga	1447		

aaacagptata atatttcataa aaagtaattt cctttttttt tttttataaa gtaaaaaattt 1597
 ttctttatac gcttgcattttt ggttaaaaagg atgacttaata gaaaaaaaaa tgaatgaanaa 1597
 ggagagattt taagaactta agactacttt ggagttttt gtaaaata atggactaan 1627
 ctgatgaaat aaaggttaagt actggacttg gaatatattt acattacagg gaacttaac 1626

<210> 20
 <211> 302
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Ala Asp Ser Ser Phe Arg Phe Pro Arg Thr Trp Trp Gln Ser Ala
 1 5 10 15
 Glu Asp Val His Arg Glu Lys Ile Gln Leu Asp Leu Glu Ala Glu Phe
 20 25 30
 Tyr Phe Thr His Leu Ile Val Met Phe Lys Ser Pro Arg Pro Ala Ala
 35 40 45
 Met Val Leu Asp Arg Ser Gln Asp Phe Gly Lys Thr Trp Lys Pro Tyr
 50 55 60
 Lys Tyr Phe Ala Thr Asn Cys Ser Ala Thr Phe Gly Leu Glu Asp Asp
 65 70 75 80
 Val Val Lys Lys Gly Ala Ile Cys Thr Ser Lys Tyr Ser Ser Pro Phe
 85 90 95
 Pro Cys Thr Gly Gly Glu Val Ile Phe Lys Ala Leu Ser Pro Pro Tyr
 100 105 110
 Arg Thr Ser Asn Pro Tyr Ser Ala Lys Val Thr Ser Val Leu Lys Ile
 115 120 125
 Thr Asn Leu Arg Val Gln Leu Leu Lys Asn Thr Ser Tyr Pro Cys Gln
 130 135 140
 Arg Asn Asp Leu Asn Glu Glu Pro Gln His Ile Thr His Tyr Ala Ile
 145 150 155 160
 Tyr Asp Phe Ile Val Lys Gly Ser Cys Phe Cys Asn Gly His Ala Asp
 165 170 175

tat gat gat gat aat aag aag tgg gtg cca gct ggt ggc tta aat gga	335
Tyr Asp Asp Ala Asn Lys Lys Trp Val Pro Ala Gly Gly Ser Thr Gly	
20 25 30	
ttc agc aga gtt cat atc tat cac cat aca ggc aac aac aca ttc aga	383
Phe Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg	
35 40 45	
gtg gtg ggc agg aag att cag gac cat cag gtc gtg ata aac tgt gcc	431
Val Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala	
50 55 60	
att cct aaa ggg ttg aag tac aat caa gct aca cag acc ttc cac cag	479
Ile Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln	
65 70 75	
tgg cga gat got aga cag gtg tat ggt ctc aac ttt ggc agc aaa gag	527
Trp Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu	
80 85 90 95	
gat gcc aat gtc ttc gca agt gcc atg atg cat gcc tta gaa gtg tta	575
Asp Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu	
100 105 110	
aat tca cag gaa aca ggg caa aca ttg cct aga caa aac tca caa cta	623
Asn Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu	
115 120 125	
cct gct caa gtt caa aat ggc caa tcc caa gaa gaa ttg gaa att caa	671
Pro Ala Gln Val Gln Asn Gly Pro Ser Gln Gln Glu Leu Glu Ile Gln	
130 135 140	
aga aga caa cta caa gaa cag caa cgg caa aag gag ctg gag cgg gaa	719
Arg Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu	
145 150 155	
agg ctg aag aga gaa aga atg gaa aga gaa agg aag aag aga gag agg	767
Arg Leu Lys Arg Glu Arg Met Glu Arg Glu Arg Lys Lys Arg Glu Arg	
160 165 170 175	
tta gaa agg gaa agg ctg gag agg gag cga ctg gaa caa gaa cag ctg	815
Leu Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu	
180 185 190	
gag aga gag aga caa gaa cgg gaa cgg cag gaa cgc ctg gag cgg cag	863
Glu Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln	
195 200 205	

gaa agt atg gag gag gaa gag atg gag gag agt cag gaa agt atg gag	111
Glu Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp	
210 215 220	
egg gag agt caa gaa aga gaa gaa aga gag agt atg gag aga atg gaa	221
Arg Glu Arg Gln Glu Arg Gln Glu Arg Glu Arg Leu Glu Arg Leu Glu	
225 230 235	
egg gag agt caa gaa agt gag aga caa gag cag tta gaa agt gaa gag	1097
Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Gln Leu Glu Arg Glu Gln	
240 245 250 255	
atg gaa tgg gag aga gag agt aga ata tca agt ggt ggt ggt ggt ggt	1055
Leu Glu Trp Glu Arg Glu Arg Arg Ile Ser Ser Ala Ala Ala Pro Ala	
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Ser Val Glu Thr Pro Leu Asn Ser Val Leu Gly Asp Ser Ser Ala Ser	
275 280 285	
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Glu Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Thr Pro Ser Gln	
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cag gaa gag aat agt ggt ata aat gga att gca ggt gca att gcc gga	1197
Gln Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala Gly	
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gca aaa att agt aaa atg tca cgg atg gag gat acc tet ttc cca agt	1247
Ala Lys Leu Arg Lys Val Ser Arg Met Glu Asp Thr Ser Phe Pro Ser	
320 325 330 335	
gga gag aat ggt att ggt gtg aac tcc gcc tca tet aaa aca gat gca	1295
Gly Gly Asn Ala Ile Gly Val Asn Ser Ala Ser Ser Lys Thr Asp Thr	
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ggc att gga aat gga acc att att tta ggg ggt agt ggt tta atg gaa	1343
Gly Arg Gly Asn Gly Pro Leu Pro Leu Gly Gly Ser Gly Leu Met Glu	
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Glu Met Ser Ala Leu Leu Ala Thr Arg Arg Arg Ile Ala Glu Lys Gly	
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Ser Thr Ile Glu Thr Glu Gln Lys Gln Asp Lys Gly Glu Asp Ser Glu	
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 Pro Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg
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 Lys Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val
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 Ile Ser Arg Pro Pro Arg Lys Asn Gln Ile Val Phe Asp Asn Arg Ser
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 Tyr Asp Ser Leu His Arg Pro Lys Ser Thr Pro Val Ile Thr Ala Gln
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 Cys Gln Trp Ser Pro Asp Gly Arg Thr
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caatcaggca ggaactgagc aagtcacata ctgcatagag gaacagacta aggagagata 1798

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Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg Val

35 40 45

Val Gly Arg Lys Ile Gln Arg His Val Val Ile Asn Cys Ala Ile
50 55 60

Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln Trp
65 70 75 80

Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu Asp
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Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu Asn
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Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu Pro
115 120 125

Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln Arg
130 135 140

Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu Arg
145 150 155 160

Leu Lys Arg Glu Arg Met Glu Arg Glu Arg Lys Lys Arg Glu Arg Leu
165 170 175

Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu
180 185 190

Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu
195 200 205

Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp Arg
210 215 220

Glu Arg Gln Glu Arg Gln Glu Arg Gln Arg Leu Glu Arg Leu Glu Arg
225 230 235 240

Gln Arg Gln Glu Arg Gln Arg Gln Glu Leu Glu Arg Gln Gln Leu
245 250 255

Gln Trp Glu Arg Glu Arg Arg Ile Ser Ser Ala Ala Ala Pro Ala Ser
260 265 270

Val Glu Thr Pro Leu Asn Ser Val Leu Gly Asp Ser Ser Ala Ser Glu
275 280 285

Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Thr Pro Ser Gln Gln
290 295 300

Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala Gly Ala
305 310 315 320

Lys Leu Arg Lys Val Ser Arg Met Glu Asp Thr Ser Phe Pro Ser Gly
325 330 335

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340 345 350

Arg Gly Asn Gly Pro Leu Pro Leu Gly Gly Ser Gly Leu Met Glu Glu
355 360 365

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370 375 380

Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu Pro
385 390 395 400

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405 410 415

Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val Ile
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Glu Arg Glu Arg Gln Glu Arg Glu Arg Gln Glu Arg Leu Glu Arg Gln				
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gaa cgc ctg gag cgg cag gaa cgc ctg gag cgg cag gaa cgc ctg gat				911
Glu Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp				
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Ser Val Glu Thr Pro Leu Asn Ser Val Leu Gly Asp Ser Ser Ala Ser				
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Gln Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala Gly				
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Ala Lys Leu Arg Lys Val Ser Arg Met Glu Asp Thr Ser Thr Leu Ser				
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Ser Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu			
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cct gta aat tct aag ggc tct tca aca agt aca cct gaa cca aca aga			1487
Pro Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg			
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atc tcc aga cca aaa tcc aca ccc tta tca cag ccc agt gcc aat gga			1583
Ile Ser Arg Pro Lys Ser Thr Pro Leu Ser Gln Pro Ser Ala Asn Gly			
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gtc cag acg gaa gga ctt gac tat gac agg ctg aag cag gac att tta			1631
Val Gln Thr Glu Gly Leu Asp Tyr Asp Arg Leu Lys Gln Asp Ile Leu			
450	455	460	
gat gaa atg aga aaa gaa tta aca aag cta aaa gaa gag ctc att gat			1679
Asp Glu Met Arg Lys Glu Leu Thr Lys Leu Lys Glu Glu Ile Ile Asp			
465	470	475	
gca atc agg cag gaa ctg agc aag tca aat act gca tagaggaaca			1725
Ala Ile Arg Gln Glu Leu Ser Lys Ser Asn Thr Ala			
480	485	490	
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Ser Arg Val His Ile Tyr His His Thr Gly Asn Asn Thr Phe Arg Val
35 40 45

Val Gly Arg Lys Ile Gln Asp His Gln Val Val Ile Asn Cys Ala Ile
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Pro Lys Gly Leu Lys Tyr Asn Gln Ala Thr Gln Thr Phe His Gln Trp
65 70 75 80

Arg Asp Ala Arg Gln Val Tyr Gly Leu Asn Phe Gly Ser Lys Glu Asp
85 90 95

Ala Asn Val Phe Ala Ser Ala Met Met His Ala Leu Glu Val Leu Asn
100 105 110

Ser Gln Glu Thr Gly Pro Thr Leu Pro Arg Gln Asn Ser Gln Leu Pro
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Ala Gln Val Gln Asn Gly Pro Ser Gln Glu Glu Leu Glu Ile Gln Arg
130 135 140

Arg Gln Leu Gln Glu Gln Gln Arg Gln Lys Glu Leu Glu Arg Glu Arg
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Leu Lys Arg Glu Arg Met Glu Arg Glu Arg Lys Lys Arg Glu Arg Leu
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Glu Arg Glu Arg Leu Glu Arg Glu Arg Leu Glu Gln Glu Gln Leu Glu
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195 200 205

Arg Leu Glu Arg Gln Glu Arg Leu Glu Arg Gln Glu Arg Leu Asp Arg
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Glu Arg Gln Glu Arg Glu Arg Gln Glu Gln Leu Glu Arg Glu Gln Leu
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Glu Trp Glu Arg Glu Arg Arg Ile Ser Ser Ala Ala Ala Pro Ala Ser
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Val Glu Thr Pro Leu Asn Ser Val Leu Gly Asp Ser Ser Ala Ser Glu
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Pro Gly Leu Gln Ala Ala Ser Gln Pro Ala Glu Thr Pro Ser Gln Gln
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Glu Asp Asn Arg Pro Leu Thr Gly Leu Ala Ala Ala Ile Ala Gly Ala
 305 310 315 320

Lys Leu Arg Lys Val Ser Arg Met Glu Asp Thr Ser Phe Pro Ser Gly
 325 330 335

Gly Asn Ala Ile Gly Val Asn Ser Ala Ser Ser Lys Thr Asp Thr Gly
 340 345 350

Arg Gly Asn Gly Pro Leu Pro Leu Gly Gly Ser Gly Leu Met Glu Glu
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Thr Ile Glu Thr Glu Gln Lys Glu Asp Lys Gly Glu Asp Ser Glu Pro
 385 390 395 400

Val Thr Ser Lys Ala Ser Ser Thr Ser Thr Pro Glu Pro Thr Arg Lys
 405 410 415

Pro Trp Glu Arg Thr Asn Thr Met Asn Gly Ser Lys Ser Pro Val Ile
 420 425 430

Ser Arg Pro Lys Ser Thr Pro Leu Ser Gln Pro Ser Ala Asn Gly Val
 435 440 445

Gln Thr Glu Gly Leu Asp Tyr Asp Arg Leu Lys Gln Asp Ile Leu Asp
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 Glu Cys Leu Gly Phe Ala Gly Val Leu Phe Gly Trp Pro Ser Leu Val
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 Phe Val Phe Lys Asn Glu Asp Tyr Phe Lys Asp Leu Cys Gly Pro Asp
 35 40 45 50
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 Ala Gly Pro Ile Gly Asn Ala Thr Gly Gln Ala Asp Cys Lys Ala Gln
 55 60 65
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 Asp Glu Arg Phe Ser Leu Ile Phe Thr Leu Gly Ser Phe Val Asn Asn
 70 75 80
 ttc atg aca ttc ccc act gcc tac atc ttc gcc ttc ttc aag aac aac 526
 Phe Met Thr Phe Pro Thr Gly Tyr Ile Phe Asp Arg Phe Lys Thr Thr
 85 90 95
 atg gca cgc ctc ata gcc ata ttt ttc tac aac aac gcc aca ctc atc 574
 Val Ala Arg Leu Ile Ala Ile Phe Phe Tyr Thr Thr Ala Thr Leu Ile
 100 105 110

116 Ala Phe Thr Ter Ala Ala Ser Leu 621
 117 120

118 121 124 127 130 133 136 139 142 145 148 151 154 157 160 163 166 169 172 175 178 181 184 187 190 193 196 199 202 205 208 211 214 217 220 223 226 229 232 235 238 241 244 247 250 253 256 259 262 265 268 271 274 277 280 283 286 289 292 295 298 301 304 307 310 313 316 319 322 325 328 331 334 337 340 343 346 349 352 355 358 361 364 367 370 373 376 379 382 385 388 391 394 397 400 403 406 409 412 415 418 421 424 427 430 433 436 439 442 445 448 451 454 457 460 463 466 469 472 475 478 481 484 487 490 493 496 499 502 505 508 511 514 517 520 523 526 529 532 535 538 541 544 547 550 553 556 559 562 565 568 571 574 577 580 583 586 589 592 595 598 601 604 607 610 613 616 619 622 625 628 631 634 637 640 643 646 649 652 655 658 661 664 667 670 673 676 679 682 685 688 691 694 697 700 703 706 709 712 715 718 721 724 727 730 733 736 739 742 745 748 751 754 757 760 763 766 769 772 775 778 781 784 787 790 793 796 799 802 805 808 811 814 817 820 823 826 829 832 835 838 841 844 847 850 853 856 859 862 865 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 Pro Asp Ala Gly Pro Ile Gly Asn Ala Thr Gly Gln Ala Asp Cys Lys
 50 55 60
 Ala Gln Asp Glu Arg Phe Ser Leu Ile Phe Thr Leu Gly Ser Phe Met
 65 70 75 80
 Asn Asn Phe Met Thr Phe Pro Thr Gly Tyr Ile Phe Asp Arg Phe Lys
 85 90 95
 Thr Thr Val Ala Arg Leu Ile Ala Ile Phe Phe Tyr Leu Thr Ala Thr
 100 105 110
 Leu Ile Ile Ala Phe Thr Ser Ala Ala Ser Leu
 115 120

<210> 27
 <211> 1063
 <212> DNA

<21> H. n. angiens

<22>

<23> 117

<222> (41, ... 1044)

<460> 127

ctttttttag ataacatctt ctgagtcata accagcctgg gtcccc atg atg ggt 56
Met Ile Val
1

ggg tcc cct tgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg 104
Gly Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu
5 10 15

cag ctg ggt tct acc tgc gtg gcc ttc tgg ctg gtg gct agc gtg ggc 152
Gln Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly
20 25 30 35

gcc tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc ttc 200
Ala Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe
40 45 50

tgc ttc tcc ggt acc ctg atc atc ctc atc gtg gag ctg tgc ggg ctc 248
Cys Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
55 60 65

cag gcc cgt ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc gcc 296
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala
70 75 80

tgc tat gcc gcc ctc ttc tgc ctc tgg gcc tcc atc atc tac ccc acc 344
Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr
85 90 95

acc tat ggt tgg ttc atg tcc cag ggc cgt tgg cgg gag ttc gcc acc 392
Thr Tyr Thr Thr Phe Leu Ser His Phe Arg Ser Arg Asn His Ala Ile
100 105 110 115

gac ggc acc ttc ttc ttc tgc atc gag tgt ggt ggt tac ggc acc ggc 440
Ala Ala Thr His Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr His
120 125 130

gtg gcc tgg acc cgg gcc cgg ccc ggc gag atc acc ggc tat atg gcc 488
Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala
135 140 145

acc gta ccc ggg ctg atg aag gtg ctg gag acc ttc gtc acc tgc acc 536

62

<400> 28

Met Ile Val Gly Ser Thr Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu
1 10 15

Arg Leu Leu Gln Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala
20 25 30

Ser Val Gly Ala Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr
35 40 45

Trp Cys Phe Cys Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu
50 55 60

Cys Gly Leu Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile
65 70 75 80

Thr Phe Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile
85 90 95

Tyr Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
100 105 110

His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr
115 120 125

Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly
130 135 140

Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val
145 150 155 160

Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His
165 170 175

Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Ile Ile
180 185 190

Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val
195 200

Leu Pro Ile Pro Phe Pro Ser His Leu Ser Gly Leu Ala Leu Leu Ser
210 215 220

Val Leu Leu Tyr Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe
225 230 235 240

Asp Glu Lys Tyr Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys

245	250	255
Ser Arg Ser His Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala		
260	265	270
Val Ala Ile Leu Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu		
275	280	285
Val His Ser Ala His Leu Val Phe Val Lys Val		
290	295	

<210> 29
 <211> 1890
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(1890)

<222> 29	
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Gly Ser Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly	
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tac tat aca aaa cag tat ccg gtg ttt gtg ggc cac aag cca gga cgg	96
Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg	
20 25 30	
aac acc aca cag agg cac agg ctg gac atc cag atg att atg atc atg	144
Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met	
35 40 45	
aac gga acc ctc tac att gct gct agg gac cat att tat act gtc gat	192
Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp	
50 55 60	
ata gac aca tca cac acg gaa gaa att tat tgt agc aaa aaa ctg aca	240
Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr	
65 70 75 80	
tgg aaa tct aga cag gcc gat gta gac aca tgc aga atg aag gga aaa	288
Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys	
85 90 95	
cat aag gat gag tgc cac aac ttt att aaa gtt ctt cta aag aaa aac	336

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn	
100 105 110	
gat gat gaa ttg ttt gtc tgt gga act act gaa ttc aac cct tcc tgc	384
Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys	
115 120 125	
aga aac tat aag atg gat aca ttg gaa tta ttc ggg gat gaa ttc agc	432
Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser	
130 135 140	
gga atg gcc aga tgc cca tat gat gcc aaa cat gcc aac gtt gca ctg	480
Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu	
145 150 155 160	
ttt gaa gat gga aaa cta tac tca gcc aca ggt act gac ttc ctt gcc	528
Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala	
165 170 175	
att gac gca gtc att tac cgg agt ctt gga gaa agc cct acc ctg cgg	576
Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg	
180 185 190	
acc gtc aag cac gat tca aaa tgg ttg aaa gaa cca tac ttt gtt caa	624
Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln	
195 200 205	
gcc gtg gat tac gga gat tat atc tac ttc ttt ttc agg gaa ata gca	672
Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala	
210 215 220	
gtg gag tat aac acc atg gga aag gta gtt ttc cca aga gtg gct cag	720
Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln	
225 230 235 240	
gtt ttt aag cat gat atg gga gga cct caa aga gtc atg gag aaa cag	768
Val Cys Tyr Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln	
245 250 255	
tgg aag tgg ttc atg aag gag cgt ttg aac ttt tca gtt cct gga gat	816
Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Tyr Ser Val Phe Gly Asp	
260 265 270	
tct cat ttt tat ttc aac att ctc cag gaa gtc aca gat gtg att cgt	864
Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg	
275 280 285	
atc aac ggg cgt gat gtt gtc atg gca aag ttt tct aca cct tat aac	912

Ile	Asn	Gly	Arg	Asp	Val	Val	Leu	Ala	Thr	Phe	Ser	Thr	Pro	Tyr	Asn	
290						295					300					
agg	atc	ccc	ggg	tct	gca	gtc	tgt	gcc	tat	gat	atg	ctt	gat	att	gcc	960
Ser	Ile	Pro	Gly	Ser	Ala	Val	Cys	Ala	Tyr	Asp	Met	Leu	Asp	Ile	Ala	
305					310					315					320	
agt	gtt	ttt	act	ggg	aga	ttc	aag	gaa	cag	aag	tct	cct	gat	tcg	acc	1008
Ser	Val	Phe	Thr	Gly	Arg	Phe	Lys	Glu	Gln	Lys	Ser	Pro	Asp	Ser	Thr	
				325					330						335	
tgg	aca	cca	gtt	cct	gat	gaa	cga	gtt	cct	aag	ccc	agg	cca	ggg	tgc	1056
Trp	Thr	Pro	Val	Pro	Asp	Glu	Arg	Val	Pro	Lys	Pro	Arg	Pro	Gly	Cys	
			340					345					350			
tgt	gct	ggc	tca	tcc	tcc	tta	gaa	aga	tat	gca	acc	tcc	aat	gag	ttc	1104
Cys	Ala	Gly	Ser	Ser	Ser	Leu	Glu	Arg	Tyr	Ala	Thr	Ser	Asn	Glu	Phe	
	355					360						365				
cct	gat	gat	acc	ctg	aac	ttc	atc	aag	acg	cac	ccg	ctc	atg	gat	gag	1152
Pro	Asp	Asp	Thr	Leu	Asn	Phe	Ile	Lys	Thr	His	Pro	Leu	Met	Asp	Glu	
	370					375					380					
gca	gtg	ccc	tcc	atc	ttc	aac	agg	cca	tgg	ttc	ctg	aga	aca	atg	gtc	1200
Ala	Val	Pro	Ser	Ile	Phe	Asn	Arg	Pro	Trp	Phe	Leu	Arg	Thr	Met	Val	
385					390					395					400	
aga	tac	ggc	ctt	acc	aaa	att	gca	gtg	gac	aca	gct	gct	ggg	cca	tat	1248
Arg	Tyr	Arg	Leu	Thr	Lys	Ile	Ala	Val	Asp	Thr	Ala	Ala	Gly	Pro	Tyr	
				405					410					415		
cag	aat	cac	act	gtg	gtt	ttt	ctg	gga	tca	gag	aag	gga	atc	atc	ttg	1296
Gln	Asn	His	Thr	Val	Val	Phe	Leu	Gly	Ser	Glu	Lys	Gly	Ile	Ile	Leu	
			420					425					430			
aag	ttt	ttg	ggc	aga	ata	gga	aat	agt	ggt	ttt	cta	aat	gac	agg	ctt	1344
Iys	Phe	Ile	Ala	Arg	Ile	Gly	Asn	Ser	Gly	Phe	Leu	Asn	Asp	Ser	Leu	
	435					440						445				
ttc	ctc	gag	gag	atg	agt	gtt	tac	aac	tct	gca	aaa	ttt	agt	tat	gat	1392
Phe	Leu	His	Glu	Met	Ser	Val	Tyr	Asn	Ser	Glu	Lys	Cys	Ser	Tyr	Asp	
	450					455					460					
gga	gtc	gaa	gac	aaa	agg	atc	atg	ggc	atg	cag	ctg	gac	aga	gca	agg	1440
Gly	Val	Glu	Asp	Lys	Arg	Ile	Met	Gly	Met	Gln	Leu	Asp	Arg	Ala	Ser	
465					470					475				480		
agg	tct	ctg	tat	gtt	ggg	ttc	tct	acc	tgt	gtg	ata	aag	gtt	ccc	ctt	1488

Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
485 490 495

ggg ggt tat gaa gga cat ggg aag tgt aaa aaa aac tgt att ggt taa 1536
Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
500 505 510

aga gat tta tat tgt gga tgg ata aag gaa ggt ggt gat tgt agc cat 1584
Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
515 520 525

tta tca tta aac agc aga ctg act ttt gag cag gac ata gag cgt ggc 1632
Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
530 535 540

aat aca gat ggt ctg ggg gac tgt cac aat tcc ttt gtg gca ctg aat 1680
Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
545 550 555 560

ggg cat tca agt tcc ctg ttg ccc agc aca acc aca tca gat tgg aag 1728
Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
565 570 575

gct caa gag ggg tat gag tct agg gga gga atg ctg gac tgg aag cat 1776
Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
580 585 590

ctg ctt gag tca cct gac agc aca gac cct ttg ggg gca gtg tct tca 1824
Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
595 600 605

cat aat taa caa gag aag aag gga gtg att cgg gaa agt taa cta aaa 1872
His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
610 615 620

ggg caa tca gag cta gag 1880
Gly His Arg Gln Leu Glu
625 630

<210> 3

<211> 67

<212> 187

<213> Homo sapiens

<400> 37

Gly Ser Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
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Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
20 25 30

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
35 40 45

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
50 55 60

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
65 70 75 80

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
85 90 95

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
100 105 110

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
115 120 125

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
130 135 140

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
145 150 155 160

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
165 170 175

Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
180 185 190

Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
195 200 205

Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Asn
210 215 220

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
225 230 235 240

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
245 250 255

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
260 265 270

Ser His Phe Tyr Ile Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
275 280 285

Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
290 295 300

Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
305 310 315 320

Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
325 330 335

Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
340 345 350

Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
355 360 365

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
370 375 380

Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
385 390 395 400

Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
405 410 415

Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
420 425 430

Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
435 440 445

Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
450 455 460

Gly Val Glu Asp Lys Arg Ala Ser Gly Met Gln Ser Asp Arg Ala Ser
465 470 475 480

Ser Ser Leu Tyr Val Ala Ile Ser Thr Cys Val Ile Lys Val Pro Leu
485 490 495

Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
500 505 510

Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
515 520 525

Leu Ser Ile Asn Ser Arg Leu Thr Ile His Val Asp Ile Glu Arg Gly
545 550 555

Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
560 565 570 575

Gly His Ser Ser Ser Leu Leu Ile Ser Thr Thr Thr Ser Asp Ser Thr
565 570 575

Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
580 585 590

Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
595 600 605

His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
610 615 620

Gly His Asp Gln Leu Glu
625 630

<210> 31

<211> 1356

<212> DNA

<213> Homo sapiens

<400> 31

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ggccggggccc tctccgaagt ccgcgaaggt attccctaga acacccagta cctcaacctc 120
atggagaaca acatccagat gatccaggtt gacaccttc gccacctcca ccacctggag 180
gtcctgcagt tgggcaggaa ctccatccgg cagattgagg tggggccctt caacggcctg 240
accagctca acacccctga cctgttctac aactggctc cagtctctc tagcgggggc 300
cttgaattcc tctccaggt gggggagtc tggattaga acaacccat cgaagcctc 360
ctctctctc tcttctcgc gctctctc ctctctctc tggctctc ggcctctc 420
agctctctc ctctctctc ggcctctc ggcctctc ctctctctc ggcctctc 480
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tgggcctctc ggcctctc ggcctctc ggcctctc ggcctctc ggcctctc 600
tgggcctctc ggcctctc ggcctctc ggcctctc ggcctctc ggcctctc 660
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gagctctc ggcctctc ggcctctc ggcctctc ggcctctc ggcctctc 960
gagctctc ggcctctc ggcctctc ggcctctc ggcctctc ggcctctc 1020
gagctctc ggcctctc ggcctctc ggcctctc ggcctctc ggcctctc 1080

Ser Phe His Gly Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser
 195 200 205

Ala Val Ser Leu Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu
 210 215 220

Val Glu Leu Asn Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp
 225 230 235 240

Leu Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu His Leu His His Asn
 245 250 255

Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu Ala Trp Trp Leu Arg
 260 265 270

Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly Arg Cys His Ala Pro
 275 280 285

Met His Met Arg Gly Arg Tyr Leu Val Glu Val Asp Gln Ala Ser Phe
 290 295 300

Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro Arg Asp Leu Asn Ile
 305 310 315 320

Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg Thr Pro Pro Met Ser
 325 330 335

Ser Val Lys Trp Leu Leu Pro Asn Gly Thr Val Leu Ser His Ala Ser
 340 345 350

Arg His Pro Arg Ile Ser Val Leu Asn Asp Gly Thr Leu Asn Phe Ser
 355 360 365

His Val Leu Leu Ser Asp Thr Gly Val Tyr Thr Cys Met Val Thr Asn
 370 375 380

Val Ala Gly Asn Ser Asn Ala Ser Ala Tyr Leu Asn Val Ser Thr Ala
 385 390 395 400

Glu Leu Asn Thr Ser Asn Tyr Ser Phe Phe Thr Thr Val Thr Val Glu
 405 410 415

Thr Thr Glu Ile Ser Pro Glu Asp Thr Thr Arg Lys Tyr Lys Pro Val
 415 420 425 430

Pro Thr Thr Ser Thr Gly Tyr Gln Pro Ala Tyr Thr Thr Ser Thr Thr
 435 440 445

<210> 33

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Primer

<20> 33

ggatccgggtt tcccagaaga ttctgagcca atc

33

<210> 34

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Primer

<20> 34

ctcagctggcgg tcgtggcatt tgaggtaact ttc

33

<210> 35

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Primer

<20> 35

ctcagctggcgg gcagggaaca

19

<210> 36

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Primer

<400> 36

tggaactaat gattttaa

17

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 37

gagtcctgga gaaaagctgg a

21

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 38

atgaggcagt gccctccatc

20

<210> 39

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 39

ccatctctgga tatgataa

19

<210> 40

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 40

gacatccattcccttcttctt

17

<210> 41

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 41

ccatcagcca gcagggtta

18

<210> 42

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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cttgctctcg agggtaagcc taccctaac

30

<210> 43

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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ctgtctggtc cctgatacag cgtttctaac

31

<210> 44

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

400 44

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4. and

-219- 45

(211) 39

02122 DNA.

(213) Artificial Sequence

2202

(223) Description of Artificial Sequence: Primer

$$\therefore 400 > 45$$

neuteglug aoutggg'ag aggtgggata t meggata

39

02102 46

2113 20

3122 DNA

0213: Artificial Sequence

2203

(223) Description of Artificial Sequence: Primer

(100) 46

ingcagtaac cagttcagca

20

(210) 47

(211) 20

0129 DNA

(213) Artificial Sequence

2205

22.5 Description of National Government Policies

[illegible]

107-62049 G * [Pg] : 1

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Abstract

622 LIVA

(23) *Antiformal* *Suppression*

22

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Asp Thr Pro Thr Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu

20 25 30

gac tgc agc cct gtt cac act acc ctg tca aag tca gat gcc aaa aaa 144

Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys

35 40 45

gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat aag ccg 192

Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro

50 55 60

| | |
|---|-----|
| gtg aag gag agg ggt ttg gtg gtg aag gac ctg aag ggt gag agt gtg | 240 |
| Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val | |
| 65 70 75 80 | |
| gtt att gag cat cgc agc tac tgc tgc gca aag ggc cgg gac aga cac | 288 |
| Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His | |
| 85 90 95 | |
| ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc cat ggc | 336 |
| Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly | |
| 100 105 110 | |
| tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc tca ccc | 384 |
| Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro | |
| 115 120 125 | |
| gtc tgg ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag gtc aag | 432 |
| Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr | |
| 130 135 140 | |
| ggc ctg cac gac gtg gac caa ggg tgg atg cga gct gtc agg aag cat | 480 |
| Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His | |
| 145 150 155 160 | |
| gcc aag ggc ctg cac ata gtg cat cgg ctg ctg ttt gag gac tgg act | 528 |
| Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr | |
| 165 170 175 | |
| tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata gag gag | 576 |
| Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu | |
| 180 185 190 | |
| ctg agc aag acc gtg gtc cag gta gca aag aac cag cat ttc gat ggc | 624 |
| Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly | |
| 195 200 205 | |
| ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc gtg ggc | 672 |
| Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly | |
| 210 215 220 | |
| ctc att cac atg ctg acc cac ttg gcc gag gct ctg cat cag gcc cgg | 720 |
| Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg | |
| 225 230 235 240 | |
| ctg ctg gac ctg ctg gtc atc ccg cct gcc atc acc ccc ggg acc gac | 768 |
| Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp | |
| 245 250 255 | |

cag cta tta ata tta acg cta aag gag ttt gag cag ctg gca cca gtt 816
Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val
200 265 300

ctg gat ggt tta agc ctc atg acc tac gac tac gca aca ctg tta tgg 864
Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp
275 280 235

gtt cga gcc tgc gtc cag gtc ctg gat ccc tgg ggc tca act tct atg 912
Val Arg Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met
290 295 300

gta tgg act aag cga cct cca agg atg ccc gtg agc ctg ttg tcc ggg 960
Val Trp Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly
305 310 315 320

cca ggt aca tcc aga cac tgaaggacca caggccccgg atggtgtggg 1008
Pro Gly Thr Ser Arg His
325

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35 40 45

Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro
50 55 60

Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val
65 70 75 80

Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His
85 90 95

Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly
100 105 110

Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro
115 120 125

Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr
130 135 140

Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His
145 150 155 160

Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr
165 170 175

Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu
180 185 190

Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly
195 200 205

Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly
210 215 220

Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg
225 230 235 240

Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp
245 250 255

Gln Leu Gly Met Phe Tyr His Lys Glu Phe Glu Gln Leu Ala Pro Val
260 265 270

Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ala Thr Leu Ser Trp
275 280 285

Val Arg Ala Cys Val Gln Val Leu Asp Pro Trp Gly Ser Thr Ser Met
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Pro Gly Thr Ser Arg His
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ctgtcaaaagt cagatgocaa aaaagccgcc tcaaagacgc tgctygagaa gagtcagttt 180
tcagataagc cgggtgaaga ccgggggttg gtggtgacgg acctcaaagc tgagagtgtg 240
gttcttgagc atgcagcta cctctcgaca aaggcccggg acagacactt tgctgggg 298
atg tac tgg gct atg tca ctg cac cag tgg aac agc cat ggc tac gat 346
Met Tyr Trp Ala Met Ser Leu His Gln Trp Asn Ser His Gly Tyr Asp
1 5 10 15
gtc acc aag gtc ttt ggg agc aag ttc aca cag atc tta ccc gtc tgg 384
Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp
20 25 30
ctg atg ctg aag aga cgt ggc agt gag atg ttt gag gtc aag ggc ctg 440
Leu Gln Leu Lys Arg Arg Gly Asn Gln Met Phe Gln Val Thr Gly Leu
35 40 45
cac gag gtc gac caa ggg tgg atg cga gct gtc agg aag cat gcc aag 496
His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys
50 55 60
agg ctg cac ata gtc cct agg ctg ctg ttt gag gac tgg act tac gat 538

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Leu | His | Ile | Val | Pro | Arg | Leu | Leu | Phe | Glu | Asp | Trp | Thr | Tyr | Asp | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gat | tto | cgg | aac | gtc | tta | gac | agt | gag | gat | gag | ata | gag | gag | ctg | agg | 586 |
| Asp | Phe | Arg | Asn | Val | Leu | Asp | Ser | Glu | Asp | Glu | Ile | Glu | Glu | Leu | Ser | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aag | acc | gtg | gtc | cag | gtg | gca | aag | aac | cag | cat | tto | gat | ggc | tto | gtg | 634 |
| Lys | Thr | Val | Val | Gln | Val | Ala | Lys | Asn | Gln | His | Phe | Asp | Gly | Phe | Val | |
| | | 100 | | | | | 105 | | | | | | 110 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtg | gag | gtc | tgg | aac | cag | ctg | cta | agg | cag | aag | cgc | gtg | ggc | ctc | atc | 682 |
| Val | Glu | Val | Trp | Asn | Gln | Leu | Ser | Gln | Lys | Arg | Val | Gly | Leu | Ile | | |
| | | 115 | | | | 120 | | | | | 125 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cac | atg | ctc | acc | cac | ttg | gcc | gag | gct | ctg | cac | cag | gcc | cgg | ctg | ctg | 730 |
| His | Met | Leu | Thr | His | Leu | Ala | Glu | Ala | Leu | His | Gln | Ala | Arg | Leu | Leu | |
| | 130 | | | | 135 | | | | | 140 | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gcc | ctc | ctg | gtc | atc | cgg | cct | gcc | atc | acc | ccc | ggg | acc | gac | cag | ctg | 778 |
| Ala | Leu | Leu | Val | Ile | Pro | Pro | Ala | Ile | Thr | Pro | Gly | Thr | Asp | Gln | Leu | |
| 145 | | | 150 | | | | | 155 | | | | | 160 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ggc | atg | tto | acg | cac | aag | gag | ttt | gag | cag | ctg | gcc | ccc | gtg | ctg | gat | 826 |
| Gly | Met | Phe | Thr | His | Lys | Glu | Phe | Glu | Gln | Leu | Ala | Pro | Val | Leu | Asp | |
| | | | 165 | | | 170 | | | | | | | 175 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ggc | tto | agg | ctc | atg | acc | tac | gac | tac | gca | aca | ctg | tcc | tgg | gtt | cga | 874 |
| Gly | Phe | Ser | Leu | Met | Thr | Tyr | Asp | Tyr | Ala | Thr | Leu | Ser | Trp | Val | Arg | |
| | | 180 | | | | 185 | | | | | | | 190 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gcc | tgc | gtc | cag | gtc | ctg | gat | ccc | tgg | ggc | tca | act | tct | atg | gta | tgg | 922 |
| Ala | Cys | Val | Gln | Val | Leu | Asp | Pro | Trp | Gly | Ser | Thr | Ser | Met | Val | Trp | |
| | 195 | | | | 200 | | | | | 205 | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| act | acg | cga | cct | cca | agg | atg | ccc | gtg | agg | ctg | ttg | tgg | ggg | cca | ggc | 970 |
| Thr | Thr | Arg | Pro | Pro | Arg | Met | Pro | Val | Ser | Leu | Leu | Ser | Gly | Pro | Gly | |
| | 210 | | | | 215 | | | | 220 | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|------|-----|-----|------|-----|-----|-----|------|------|----|------|
| aca | tcc | aga | cac | tga | agg | acca | cag | gcc | ccgg | atg | gtg | ggg | acgg | ccag | gc | 1012 |
| Thr | Ser | Arg | His | | | | | | | | | | | | | |
| 225 | | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|-----|----|-----|----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|------|
| ctc | ag | agc | ac | ttc | ctg | agc | atg | aca | aga | ag | cag | agg | acg | ctg | tct | ctc | 1052 |
| | | | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|----|----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|------|
| aac | cct | ga | ag | tcc | ctg | cag | tgc | ggc | ctg | ga | ctg | ggc | ccg | gag | ctg | ggg | ctc | 1142 |
| | | | | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|----|-----|-----|-----|-----|----|----|----|----|----|-----|-----|-----|-----|-----|------|
| nat | gtg | ggg | ag | ctg | ggc | cag | gct | gg | ac | ta | ag | ac | ctg | ctc | ctg | ggc | ctg | 1202 |
| | | | | | | | | | | | | | | | | | | |

Ala Tyr Val His Val Leu Asp Pro Trp Gly Ser Thr Ser Met Val Trp
195 200 205

Thr Thr Arg Pro Pro Arg Met Pro Val Ser Leu Leu Ser Gly Pro Gly
215 220

Thr Ser Arg His
225

<210> 78

<211> 816

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)...(628)

<400> 78

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Arg Val Leu Val Leu Met Val Gly Ala Val Met Phe Thr Arg Gly Ser
1 5 10 15

cgg gcc gcc tgg ggg cgc gcc agg gag aat atc tgc ttg ctc aac ttc 97
Pro Ala Ala Trp Gly Arg Ala Arg Glu Asn Ile Cys Leu Leu Asn Phe
20 25 30

ttc tct ggc acc atc gtg ctc atc ttc ttc ctg gag ctg gct gtg gcc 145
Phe Cys Gly Thr Ile Val Leu Ile Phe Phe Leu Glu Leu Ala Val Ala
35 40 45

gtg ctg gcc ttc ctg ttc cag gac tgg gtg agg gac cgg ttc cgg gag 193
Val Leu Ala Phe Leu Phe Gln Asp Trp Val Arg Asp Arg Phe Arg Glu
50 55 60

tta tta gag ggt aac atc aag ttc tac tgg gac ggt aac ttc ctg ttc 241
Thr Thr Gln Ser Asn Ile Lys Ser Tyr Arg Asp Asp Ile Asp Leu Gln
65 70 75 80

aac ctg atc gac tcc ctt cag aaa gct aac cag tgc tgt gcc gcc tat 289
Asn Leu Ile Asp Ser Leu Gln Lys Ala Asn Gln Cys Cys Gly Ala Tyr
85 90 95

ggc cct gaa gac tgg gac ctc aac gtc tac ttc aat tgc aac ggt gcc 337
Gly Pro Gln Asp Trp Asp Leu Asn Val Tyr Phe Asn Cys Ser Gly Ala
100 105 110

agg tac aac tga gag aag tgc ggg gtc acc ttc tcc tgc tgc gag aca 385
 Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser Cys Cys Val Pro
 115 120 125

gat cct gag aca aaa gtt gtg aac aca cag tgt gga tat gat gtc agg 433
 Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly Tyr Asp Val Arg
 130 135 140

att cag ctg aag agc aag tgg gat gag tcc atc ttc acg aaa ggc tgc 481
 Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser Ile Phe Thr Lys Gly Cys
 145 150 155 160

atc cag gcc ctg gaa agc tgg ctc ccc cgg aac att tac att gtg got 529
 Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile Tyr Ile Val Ala
 165 170 175

ggc gtc ttc atc gcc atc tgg ctg ttg cag ata ttt ggc atc ttc ctg 577
 Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe Gly Ile Phe Leu
 180 185 190

gca agg acg ctg atc tca gac atc gag gca gtg aag gcc ggc cat cac 625
 Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys Ala Gly His His
 195 200 205

tcc tgaggagcag agttagggga gcagagctga gccacgctgg gagggccagag 678
 Phe

cctttctctg ccacagccc tacgtccaga gggagaggag ccgacacccc cagagccagt 738

gcccacatctt aagcatcagc gtgaactgac ctctctgttt ctgcttctg gtgctgaaga 798

ccaagggctcc cccctgtt 816

<210> 79

<211> 209

<212> PHE

<213> Homo sapiens

<430> 79

Arg Val Leu Val Leu Met Val Gly Ala Val Met Phe Thr Arg Gly Ser
 1 5 10 15

Pro Ala Ala Tyr Gly Arg Ala Arg Glu Asn Ile Cys Leu Leu Asn Phe
 20 25 30

Phe Cys Gly Thr Ile Val Leu Ile Phe Phe Leu Glu Leu Ala Val Ala

| | | |
|---|-----|-----|
| 35 | 40 | 45 |
| Val Leu Ala Phe Ser Phe Gln Asp Trp Val Arg Asp Arg Phe Arg Gln | | |
| 50 | 55 | 60 |
| Phe Phe Glu Ser Asn Ile Lys Ser Tyr Arg Asp Asp Ile Asp Leu Gln | | |
| 65 | 70 | 75 |
| Asn Leu Ile Asp Ser Leu Gln Lys Ala Asn Gln Cys Cys Gly Ala Tyr | | |
| 85 | 90 | 95 |
| Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr Phe Asn Cys Ser Gly Ala | | |
| 100 | 105 | 110 |
| Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser Cys Cys Val Pro | | |
| 115 | 120 | 125 |
| Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly Tyr Asp Val Arg | | |
| 130 | 135 | 140 |
| Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser Ile Phe Thr Lys Gly Cys | | |
| 145 | 150 | 155 |
| Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile Tyr Ile Val Ala | | |
| 165 | 170 | 175 |
| Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe Gly Ile Phe Leu | | |
| 180 | 185 | 190 |
| Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys Ala Gly His His | | |
| 195 | 200 | 205 |
| Phe | | |

<210> 80

<211> 1574

<212> DNA

<213> Homo sapiens

<210>

<221> CDS

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<400> 80

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| Met Ser Asn Pro Ser Ala Pro Pro Tyr Glu Asp Arg Asn Pro | |
| 1 5 10 15 | |
| ctg tac cca ggc ccc atg ttc ttc ggg ggc tat ggg cag cca tct gtc | 198 |
| Leu Tyr Pro Gly Pro Leu Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val | |
| 20 25 30 | |
| ctg cca gga ggg tat cct gcc tac cct gcc tac ccg cag cct gcc tac | 203 |
| Leu Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr | |
| 35 40 45 | |
| ggc cac cct gct ggc tac cca cag ccc atg ccc ccc acc cac ccg atg | 251 |
| Gly His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met | |
| 50 55 60 | |
| ccc atg aac tac ggc cca ggc cat ggc tat gat ggg gag gag aga gcc | 299 |
| Pro Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala | |
| 65 70 75 | |
| gtg agt gat agc ttc ggg cct gga gag tgg gat gac cgg aaa gtg cga | 347 |
| Val Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg | |
| 80 85 90 95 | |
| cac act ttt atc cga aag gtt tac tcc atc atc tcc gtg cag ctg ctc | 395 |
| His Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu | |
| 100 105 110 | |
| atc act gtg gcc atc att gct atc ttc acc ttt gtg gaa cct gtc agc | 443 |
| Ile Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser | |
| 115 120 125 | |
| gcc ttt gtg agg aga aat gtg gct gtc tac tac gtg tcc tat gct gtc | 491 |
| Ala Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val | |
| 130 135 140 | |
| ttc gtt gtc aac tac atg ttc ttc gtt ttt tgc ttc ggc ttc aga tgc | 539 |
| Phe Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Ala Gly Pro Arg Arg | |
| 145 150 155 | |
| agt ttc cca tgg aac atc att ctt ctg aac att ttt act ttt gcc atg | 587 |
| Arg Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met | |
| 160 165 170 175 | |
| ggc ttc atg acg ggc acc att tcc agt atg tac aac acc aaa gcc gtc | 635 |
| Gly Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val | |
| 180 185 190 | |

atc att gca arg atc atc att ggg ggg ggg ggg att tca gtc aac atc 673
 Ile Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile
 195 200 205

ttc tgc ttt tag aac aag tgg agg gga tgg agg ggt gtt ccc tgg ccc 761
 Phe Cys Phe Gln Thr Lys Val Arg Ala Trp Arg Ala Leu Pro Trp Pro
 210 215 220

ccc gac tcc cct ttc tta tca ggc ccg gac ccc ggt aca cta ggg atg 779
 Pro Asp Ser Pro Phe Leu Ser Gly Pro Asp Pro Gly Thr Leu Gly Met
 225 230 235

ttc cct aga gac ctg atc ccc ttc tca tca tcc gca cct aca aac ctg 827
 Phe Pro Arg Asp Leu Ile Pro Phe Ser Ser Ser Ala Pro Thr Lys Leu
 240 245 250 255

tgt cct gtt tct gtc ctt aga atg ttg tgg aca ttc cca tac ccc cta 875
 Cys Pro Val Ser Val Leu Arg Met Leu Trp Thr Phe Pro Tyr Pro Leu
 260 265 270

gga ggc agc act ggg act ccc tgg cag ggc cag tct gac tgg gct ggt 923
 Gly Gly Ser Thr Gly Thr Pro Trp Gln Gly Gln Ser Asp Trp Ala Gly
 275 280 285

tgt cac agc cat ctg aca ggt gcc tct ttc ttg ctt cct ggc agg tgg 971
 Cys His Ser His Leu Thr Gly Ala Ser Phe Leu Leu Pro Gly Arg Trp
 290 295 300

act tca cct cgt gca cag gcc tct tct ggg tcc tgg gaa ttg tgc tcc 1019
 Thr Ser Pro Arg Ala Gln Ala Ser Ser Val Ser Trp Glu Leu Cys Ser
 305 310 315

tgg tgactgggat tgtaactaga attgtgctct tagcattggt ctctacttcc 1072
 Trp
 320

aatagttta tgggttaa atgtctat tgggtggg ggtattat ttcaattgt 1132

tcttgggtta tgaacatag ctgggtctgg ggaatggg gaaacatt agtctagagg 1192

actaataaa tggggatg cagttttaa agatctat ctatattt acatttgtg 1232

tgcagctgat gggggatgg aattaaggag caagatcca tttaacccg attctgggct 1312

ctcccttcca atctagaggg ctgggtctaa tgactgtgtt ctgggttta ggccctttt 1372

ctccctctg aataaatga ccagtctct ctctctctg ggaacaggtg gctctctgg 1432

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2574

<210> 61
 <211> 320
 <212> FRT
 <213> Homo sapiens

<400> 61

Met Ser Asn Pro Ser Ala Pro Pro Pro Tyr Glu Asp Arg Asn Pro Leu
1 5 10 15

Tyr Pro Gly Pro Leu Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu
20 25 30

Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr Gly
35 40 45

His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro
50 55 60

Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val
65 70 75 80

Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His
85 90 95

Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu Ile
100 105 110

Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser Ala
115 120 125

Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe
130 135 140

Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg
145 150 155 160

Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly
165 170 175

Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile
180 185 190

Ile Ala Thr Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe
195 200 205

Cys Ile Ala Thr Lys Val Arg Ala Trp Arg Ala Leu Pro Trp Pro Pro
210 215 220

Asp Ser Pro Phe Leu Ser Gly Pro Asp Pro Gly Thr Leu Gly Met Phe
225 230 235 240

Pro Arg Asp Leu Ile Pro Phe Ser Ser Ser Ala Pro Thr Lys Leu Cys
245 250 255

Pro Val Ser Val Leu Arg Met Leu Trp Thr Phe Pro Tyr Trp Leu Gly
 261 265 271

Gly Ser Thr Gly Thr Pro Trp Gln Gly Gln Ser Asp Trp Ala Gly Cys
 277 280 285

His Ser His Leu Thr Gly Ala Ser Phe Leu Leu Pro Gly Arg Trp Thr
 290 295 300

Ser Pro Arg Ala Gln Ala Ser Ser Val Ser Trp Glu Leu Cys Ser Trp
 305 310 315 320